

SEQUENCE LISTING

<110> Andre R. Abad
 Nicholas B. Duck
 Xiang Feng
 Ronald D. Flannagan
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 Lynn E. Sims

<120> Genes Encoding Novel Proteins With
 Pesticidal Activity Against Coleopterans

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Ser Trp Tyr Asp Lys Ala Pro Ser Phe Gly Val Ile Glu Ser Ser Val	
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Ile Arg Pro Pro His Val Phe Asp Tyr Ile Thr Gly Leu Thr Val Tyr	
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Gly His Gln Ile Ser Tyr His Arg Ile Phe Ser Asp Asn Ile Ile Lys	
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Gln Met Tyr Gly Thr Asn Gln Asn Leu His Ser Thr Ser Thr Phe Asp	
385 390 395 400	
ttt acg aat tat gat att tac aag acg tta tca aaa gat gcg gtg ctc	1248
Phe Thr Asn Tyr Asp Ile Tyr Lys Thr Leu Ser Lys Asp Ala Val Leu	
405 410 415	
ctt gat att gtt ttt cct ggt tat acg tat ata ttt ttt gga atg cca	1296
Leu Asp Ile Val Phe Pro Gly Tyr Thr Tyr Ile Phe Phe Gly Met Pro	
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Glu Val Glu Phe Phe Met Val Asn Gln Leu Asn Asn Thr Arg Lys Thr	
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Leu Lys Tyr Asn Pro Val Ser Lys Asp Ile Ile Ala Gly Thr Arg Asp	

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Ser Tyr Ser His Arg Leu Cys His Ile Thr Ser Ile Pro Ala Thr Gly			
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Ser Thr Thr Gly Leu Val Pro Val Phe Ser Trp Thr His Arg Ser Ala			
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Asp Leu Ile Asn Ala Val His Ser Asp Lys Ile Thr Gln Ile Pro Val			
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Val Lys Val Ser Asp Leu Ala Pro Ser Ile Thr Gly Gly Pro Asn Asn			
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Thr Glu Phe Tyr Ile Asn Pro Ser Glu Glu Asn Val Lys Ser His Ala			
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Gln Lys Thr Met Asn Arg Gly Glu Ala Leu Thr Tyr Asn Lys Phe Asn			
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Thr Leu Gly Ala Ile Phe Glu Ala Glu Asp Phe Leu Gly Ile Glu Ala			
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Tyr Ile Asp Arg Ile Glu Phe Ile Pro Val Asp Glu Thr Tyr Glu Ala			
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Glu Gln Asp Leu Glu Ala Ala Lys Lys Ala Val Asn Ala Leu Phe Thr			
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Asn Thr Lys Asp Gly Leu Arg Pro Gly Val Thr Asp Tyr Glu Val Asn			
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Gln Ala Ala Asn Leu Val Glu Cys Leu Ser Asp Asp Leu Tyr Pro Asn	
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Val Lys Asn Val Pro Asp Asp Leu Leu Pro Asp Val Ser Pro Val Asn	
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Ser Asp Gly Ser Ile Asn Arg Cys Ser Glu Gln Lys Tyr Val Asn Ser	
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 Thr Gln Leu Ile Asp Ile Leu Trp Pro Ser Gly Gln Lys Ser Gln Trp
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 115 120 125
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 355 360 365
 Gly His Gln Ile Ser Tyr His Arg Ile Phe Ser Asp Asn Ile Ile Lys
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 Gln Met Tyr Gly Thr Asn Gln Asn Leu His Ser Thr Ser Thr Phe Asp
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 Pro Thr Asn Ala Leu Gln Asn Met Asp Tyr Lys Asp Tyr Leu Lys Met
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 tct gcg gga aat gct agt gaa tac cct ggt tca cct gaa gta ctt gtt 192

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Thr Gln Ser Arg Ser Ile Ser Ser Ala Arg Tyr Ile Arg His Trp Ala	
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Gly His Gln Ile Ser Tyr His Arg Val Ser Arg Gly Ser Asn Leu Gln	
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Gln Met Tyr Gly Thr Asn Gln Asn Leu His Ser Thr Ser Thr Phe Asp	
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Ser Tyr Ser His Arg Leu Cys His Ile Thr Ser Ile Pro Ala Thr Gly	
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Gly Lys Tyr Arg Val Arg Leu Arg Tyr Ala Thr Asp Ala Asp Ile Val
580 585 590

ttg cat gta aac gat gct cag att cag atg cca aaa aca atg aac cca 1824
Leu His Val Asn Asp Ala Gln Ile Gln Met Pro Lys Thr Met Asn Pro
595 600 605

ggt gag gat ctg aca tct aaa act ttt aaa gtt gca gat gct atc aca 1872
Gly Glu Asp Leu Thr Ser Lys Thr Phe Lys Val Ala Asp Ala Ile Thr
610 615 620

aca tta aat tta gca aca gat agt tcg cta gca ttg aaa cat aat tta 1920
Thr Leu Asn Leu Ala Thr Asp Ser Ser Leu Ala Leu Lys His Asn Leu
625 630 635 640

ggt gaa gac cct aat tca aca tta tct ggt ata gtt tac gtt gac cga 1968
Gly Glu Asp Pro Asn Ser Thr Leu Ser Gly Ile Val Tyr Val Asp Arg
645 650 655

atc gaa ttc atc cca gta gat gag aca tat gaa gc 2003
Ile Glu Phe Ile Pro Val Asp Glu Thr Tyr Glu
660 665

<210> 6
<211> 667
<212> PRT
<213> Bacillus thuringiensis (truncated)

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35 40 45
Ser Ala Gly Asn Ala Ser Glu Tyr Pro Gly Ser Pro Glu Val Leu Val
50 55 60
Ser Gly Gln Asp Ala Ala Lys Ala Ala Ile Asp Ile Val Gly Lys Leu
65 70 75 80
Leu Ser Gly Leu Gly Val Pro Phe Val Gly Pro Ile Val Ser Leu Tyr
85 90 95
Thr Gln Leu Ile Asp Ile Leu Trp Pro Ser Gly Glu Lys Ser Gln Trp
100 105 110
Glu Ile Phe Met Glu Gln Val Glu Glu Leu Ile Asn Gln Lys Ile Ala
115 120 125
Glu Tyr Ala Arg Asn Lys Ala Leu Ser Glu Leu Glu Gly Leu Gly Asn
130 135 140
Asn Tyr Gln Leu Tyr Leu Thr Ala Leu Glu Glu Trp Glu Glu Asn Pro
145 150 155 160
Asn Gly Ser Arg Ala Leu Arg Asp Val Arg Asn Arg Phe Glu Ile Leu
165 170 175
Asp Ser Leu Phe Thr Gln Tyr Met Pro Ser Phe Arg Val Thr Asn Phe
180 185 190
Glu Val Pro Phe Leu Thr Val Tyr Ala Met Ala Ala Asn Leu His Leu
195 200 205
Leu Leu Leu Lys Asp Ala Ser Ile Phe Gly Glu Glu Trp Gly Trp Ser

210	215	220
Thr Thr Thr Ile Asn Asn Tyr Tyr Asp Arg Gln Met Lys Leu Thr Ala		
225	230	235
Glu Tyr Ser Asp His Cys Val Lys Trp Tyr Glu Thr Gly Leu Ala Lys		
	245	250
Leu Lys Gly Thr Ser Ala Lys Gln Trp Val Asp Tyr Asn Gln Phe Arg		
	260	265
Arg Glu Met Thr Leu Ala Val Leu Asp Val Val Ala Leu Phe Pro Asn		
	275	280
Tyr Asp Thr Arg Thr Tyr Pro Met Glu Thr Lys Ala Gln Leu Thr Arg		
	290	295
Glu Val Tyr Thr Asp Pro Leu Gly Ala Val Asn Val Ser Ser Ile Gly		
305	310	315
Ser Trp Tyr Asp Lys Ala Pro Ser Phe Gly Val Ile Glu Ser Ser Val		
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Ile Arg Pro Pro His Val Phe Asp Tyr Ile Thr Gly Leu Thr Val Tyr		
	340	345
Thr Gln Ser Arg Ser Ile Ser Ser Ala Arg Tyr Ile Arg His Trp Ala		
	355	360
Gly His Gln Ile Ser Tyr His Arg Val Ser Arg Gly Ser Asn Leu Gln		
	370	375
Gln Met Tyr Gly Thr Asn Gln Asn Leu His Ser Thr Ser Thr Phe Asp		
385	390	395
Phe Thr Asn Tyr Asp Ile Tyr Lys Thr Leu Ser Lys Asp Ala Val Leu		
	405	410
Leu Asp Ile Val Tyr Pro Gly Tyr Thr Tyr Ile Phe Phe Gly Met Pro		
	420	425
Glu Val Glu Phe Phe Met Val Asn Gln Leu Asn Asn Thr Arg Lys Thr		
	435	440
Leu Lys Tyr Asn Pro Val Ser Lys Asp Ile Ile Ala Ser Thr Arg Asp		
	450	455
Ser Glu Leu Glu Leu Pro Pro Glu Thr Ser Asp Gln Pro Asn Tyr Glu		
465	470	475
Ser Tyr Ser His Arg Leu Cys His Ile Thr Ser Ile Pro Ala Thr Gly		
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Asn Thr Thr Gly Leu Val Pro Val Phe Ser Trp Thr His Arg Ser Ala		
	500	505
Asp Leu Asn Asn Thr Ile Tyr Ser Asp Lys Ile Thr Gln Ile Pro Ala		
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Val Lys Cys Trp Asp Asn Leu Pro Phe Val Pro Val Val Lys Gly Pro		
	530	535
Gly His Thr Gly Gly Asp Leu Leu Gln Tyr Asn Arg Ser Thr Gly Ser		
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Val Gly Thr Leu Phe Leu Ala Arg Tyr Gly Leu Ala Leu Glu Lys Ala		
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Gly Lys Tyr Arg Val Arg Leu Arg Tyr Ala Thr Asp Ala Asp Ile Val		
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Leu His Val Asn Asp Ala Gln Ile Gln Met Pro Lys Thr Met Asn Pro		
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Gly Glu Asp Leu Thr Ser Lys Thr Phe Lys Val Ala Asp Ala Ile Thr		
	610	615
Thr Leu Asn Leu Ala Thr Asp Ser Ser Leu Ala Leu Lys His Asn Leu		
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Gly Glu Asp Pro Asn Ser Thr Leu Ser Gly Ile Val Tyr Val Asp Arg		
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Ile Glu Phe Ile Pro Val Asp Glu Thr Tyr Glu		
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<210> 7
 <211> 2003
 <212> DNA
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<220>
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 <222> (1)...(2001)

<221> misc_feature
 <222> (0)...(0)
 <223> 1218-2

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tct act tct gta tcc aat gat tct aac aga tac cct ttt gcg aat gag 96
Ser Thr Ser Val Ser Asn Asp Ser Asn Arg Tyr Pro Phe Ala Asn Glu
20 25 30

cca aca aat gcg cta caa aat atg gat tat aaa gat tat tta aaa atg 144
Pro Thr Asn Ala Leu Gln Asn Met Asp Tyr Lys Asp Tyr Leu Lys Met
35 40 45

tct gcg gga aat gct agt gaa tac cct ggt tca cct gaa gta ctt gtt 192
Ser Ala Gly Asn Ala Ser Glu Tyr Pro Gly Ser Pro Glu Val Leu Val
50 55 60

agc gga caa gat gca gct aag gcc gca att gat ata gta ggt aaa tta 240
Ser Gly Gln Asp Ala Ala Lys Ala Ala Ile Asp Ile Val Gly Lys Leu
65 70 75 80

cta tca ggt tta ggg gtc cca ttt gtt ggg ccg ata gtg agt ctt tat 288
Leu Ser Gly Leu Gly Val Pro Phe Val Gly Pro Ile Val Ser Leu Tyr
85 90 95

act caa ctt att gat att ctg tgg cct tca ggg caa aag agt caa tgg 336
Thr Gln Leu Ile Asp Ile Leu Trp Pro Ser Gly Gln Lys Ser Gln Trp
100 105 110

gag att ttt atg gaa caa gta gaa gaa ctc ata aat caa aaa ata gca 384
Glu Ile Phe Met Glu Gln Val Glu Glu Leu Ile Asn Gln Lys Ile Ala
115 120 125

gaa tat gca agg aat aaa gcg ctt tcg gaa tta gaa gga tta ggt aat 432
Glu Tyr Ala Arg Asn Lys Ala Leu Ser Glu Leu Glu Gly Leu Gly Asn
130 135 140

aat tac caa tta tat cta act gcg ctt gaa gaa tgg aaa gaa aat cca 480
Asn Tyr Gln Leu Tyr Leu Thr Ala Leu Glu Glu Trp Lys Glu Asn Pro
145 150 155 160

aat ggt tca aga gcc tta cga gat gtg cga aat cga ttt gaa atc ctg 528
Asn Gly Ser Arg Ala Leu Arg Asp Val Arg Asn Arg Phe Glu Ile Leu
165 170 175

gat agt tta ttt acg caa tac atg cca tct ttt cga gtg aca aat ttt 576
Asp Ser Leu Phe Thr Gln Tyr Met Pro Ser Phe Arg Val Thr Asn Phe
180 185 190

gaa gta cca ttc ctt aca gta tat aca cag gca gcc aac ctt cat tta 624
Glu Val Pro Phe Leu Thr Val Tyr Thr Gln Ala Ala Asn Leu His Leu
195 200 205

ctg tta tta aag gac gct tca att ttt gga gaa gaa tgg gga tgg tct 672

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Thr	Thr	Thr	Ile	Asn	Asn	Tyr	Tyr	Asp	Arg	Gln	Met	Lys	Leu	Thr	Ala		
225					230					235					240		
gaa	tat	tct	gat	cac	tgt	gta	aag	tgg	tat	gaa	act	ggc	tta	gca	aaa	768	
Glu	Tyr	Ser	Asp	His	Cys	Val	Lys	Trp	Tyr	Glu	Thr	Gly	Leu	Ala	Lys		
				245					250					255			
tta	aaa	ggc	acg	agc	gct	aaa	caa	tgg	gtc	gac	tat	aac	caa	ttc	cgt	816	
Leu	Lys	Gly	Thr	Ser	Ala	Lys	Gln	Trp	Val	Asp	Tyr	Asn	Gln	Phe	Arg		
			260					265					270				
aga	gaa	atg	aca	ctg	acg	gtt	tta	gat	gtt	gtt	gca	tta	ttc	cca	aat	864	
Arg	Glu	Met	Thr	Leu	Thr	Val	Leu	Asp	Val	Val	Ala	Leu	Phe	Pro	Asn		
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tat	gac	aca	cgc	acg	tac	cca	atg	gaa	acg	aaa	gca	caa	cta	aca	agg	912	
Tyr	Asp	Thr	Arg	Thr	Tyr	Pro	Met	Glu	Thr	Lys	Ala	Gln	Leu	Thr	Arg		
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Glu	Val	Tyr	Thr	Asp	Pro	Leu	Gly	Ala	Val	Asn	Val	Ser	Ser	Ile	Gly		
305					310					315					320		
tcc	tgg	tat	gac	aaa	gca	cct	tct	ttc	gga	gtg	ata	gaa	tca	tcc	gtt	1008	
Ser	Trp	Tyr	Asp	Lys	Ala	Pro	Ser	Phe	Gly	Val	Ile	Glu	Ser	Ser	Val		
				325					330					335			
att	cga	cca	ccc	cat	gta	ttt	gat	tat	ata	acg	gga	ctc	aca	gtg	tat	1056	
Ile	Arg	Pro	Pro	His	Val	Phe	Asp	Tyr	Ile	Thr	Gly	Leu	Thr	Val	Tyr		
			340					345					350				
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Thr	Gln	Ser	Arg	Ser	Ile	Ser	Ser	Ala	Arg	Tyr	Ile	Arg	His	Trp	Ala		
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ggc	cat	caa	ata	agc	tat	cat	cgg	att	ttt	agt	gat	aat	att	ata	aaa	1152	
Gly	His	Gln	Ile	Ser	Tyr	His	Arg	Ile	Phe	Ser	Asp	Asn	Ile	Ile	Lys		
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cag	atg	tat	gga	act	aat	caa	aat	cta	cac	agc	act	agt	acc	ttt	gat	1200	
Gln	Met	Tyr	Gly	Thr	Asn	Gln	Asn	Leu	His	Ser	Thr	Ser	Thr	Phe	Asp		
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Phe	Thr	Asn	Tyr	Asp	Ile	Tyr	Lys	Thr	Leu	Ser	Lys	Asp	Ala	Val	Leu		
				405					410					415			
ctt	gat	att	gtt	ttt	cct	ggc	tat	acg	tat	ata	ttt	ttt	gga	atg	cca	1296	
Leu	Asp	Ile	Val	Phe	Pro	Gly	Tyr	Thr	Tyr	Ile	Phe	Phe	Gly	Met	Pro		
			420					425					430				
gaa	gtc	gag	ttt	ttc	atg	gta	aac	caa	ttg	aat	aat	acc	aga	aag	acg	1344	
Glu	Val	Glu	Phe	Phe	Met	Val	Asn	Gln	Leu	Asn	Asn	Thr	Arg	Lys	Thr		
		435					440					445					
tta	aag	tat	aat	ccg	gtt	tcc	aaa	gat	att	ata	gcg	ggg	aca	aga	gat	1392	
Leu	Lys	Tyr	Asn	Pro	Val	Ser	Lys	Asp	Ile	Ile	Ala	Gly	Thr	Arg	Asp		
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Ser Tyr Ser His Arg Leu Cys His Ile Thr Ser Ile Pro Ala Thr Gly	
485 490 495	
tca act acc gga tta gta cct gta ttt tct tgg aca cat cgg agt gcc	1536
Ser Thr Thr Gly Leu Val Pro Val Phe Ser Trp Thr His Arg Ser Ala	
500 505 510	
gat ctt ata aat gca gtt cat tca gat aaa att act cag att ccg gtc	1584
Asp Leu Ile Asn Ala Val His Ser Asp Lys Ile Thr Gln Ile Pro Val	
515 520 525	
gta aag gtt tct gat ttg gct ccc tct ata aca gga ggg cca aat aat	1632
Val Lys Val Ser Asp Leu Ala Pro Ser Ile Thr Gly Gly Pro Asn Asn	
530 535 540	
acc gtt gta tcg ggt cct gga ttt aca ggg ggg ggg ata ata aaa gta	1680
Thr Val Val Ser Gly Pro Gly Phe Thr Gly Gly Gly Ile Ile Lys Val	
545 550 555 560	
ata aga aat gga gta att ata tca cat atg cgt gtt aaa att tca gac	1728
Ile Arg Asn Gly Val Ile Ile Ser His Met Arg Val Lys Ile Ser Asp	
565 570 575	
att aac aaa gaa tat agt atg agg att cgg tat gct tcc gct aat aat	1776
Ile Asn Lys Glu Tyr Ser Met Arg Ile Arg Tyr Ala Ser Ala Asn Asn	
580 585 590	
act gaa ttt tat ata aat cct tct gaa gaa aac gtt aaa tct cac gct	1824
Thr Glu Phe Tyr Ile Asn Pro Ser Glu Glu Asn Val Lys Ser His Ala	
595 600 605	
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Gln Lys Thr Met Asn Arg Gly Glu Ala Leu Thr Tyr Asn Lys Phe Asn	
610 615 620	
tat gcg act ttg ccc cct att aaa ttt acg aca acc gaa cct ttc att	1920
Tyr Ala Thr Leu Pro Pro Ile Lys Phe Thr Thr Thr Glu Pro Phe Ile	
625 630 635 640	
act cta ggg gct ata ttt gaa gcg gaa gac ttt ctt gga att gaa gct	1968
Thr Leu Gly Ala Ile Phe Glu Ala Glu Asp Phe Leu Gly Ile Glu Ala	
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<210> 8

<211> 667

<212> PRT

<213> Bacillus thuringiensis (truncated)

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Pro Thr Asn Ala Leu Gln Asn Met Asp Tyr Lys Asp Tyr Leu Lys Met
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Ser Ala Gly Asn Ala Ser Glu Tyr Pro Gly Ser Pro Glu Val Leu Val
   50         55         60
Ser Gly Gln Asp Ala Ala Lys Ala Ala Ile Asp Ile Val Gly Lys Leu
   65         70         75         80
Leu Ser Gly Leu Gly Val Pro Phe Val Gly Pro Ile Val Ser Leu Tyr
   85         90         95
Thr Gln Leu Ile Asp Ile Leu Trp Pro Ser Gly Gln Lys Ser Gln Trp
  100        105        110
Glu Ile Phe Met Glu Gln Val Glu Glu Leu Ile Asn Gln Lys Ile Ala
  115        120        125
Glu Tyr Ala Arg Asn Lys Ala Leu Ser Glu Leu Glu Gly Leu Gly Asn
  130        135        140
Asn Tyr Gln Leu Tyr Leu Thr Ala Leu Glu Glu Trp Lys Glu Asn Pro
  145        150        155        160
Asn Gly Ser Arg Ala Leu Arg Asp Val Arg Asn Arg Phe Glu Ile Leu
  165        170        175
Asp Ser Leu Phe Thr Gln Tyr Met Pro Ser Phe Arg Val Thr Asn Phe
  180        185        190
Glu Val Pro Phe Leu Thr Val Tyr Thr Gln Ala Ala Asn Leu His Leu
  195        200        205
Leu Leu Leu Lys Asp Ala Ser Ile Phe Gly Glu Glu Trp Gly Trp Ser
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Thr Thr Thr Ile Asn Asn Tyr Tyr Asp Arg Gln Met Lys Leu Thr Ala
  225        230        235        240
Glu Tyr Ser Asp His Cys Val Lys Trp Tyr Glu Thr Gly Leu Ala Lys
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Leu Lys Gly Thr Ser Ala Lys Gln Trp Val Asp Tyr Asn Gln Phe Arg
  260        265        270
Arg Glu Met Thr Leu Thr Val Leu Asp Val Val Ala Leu Phe Pro Asn
  275        280        285
Tyr Asp Thr Arg Thr Tyr Pro Met Glu Thr Lys Ala Gln Leu Thr Arg
  290        295        300
Glu Val Tyr Thr Asp Pro Leu Gly Ala Val Asn Val Ser Ser Ile Gly
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Ser Trp Tyr Asp Lys Ala Pro Ser Phe Gly Val Ile Glu Ser Ser Val
  325        330        335
Ile Arg Pro Pro His Val Phe Asp Tyr Ile Thr Gly Leu Thr Val Tyr
  340        345        350
Thr Gln Ser Arg Ser Ile Ser Ser Ala Arg Tyr Ile Arg His Trp Ala
  355        360        365
Gly His Gln Ile Ser Tyr His Arg Ile Phe Ser Asp Asn Ile Ile Lys
  370        375        380
Gln Met Tyr Gly Thr Asn Gln Asn Leu His Ser Thr Ser Thr Phe Asp
  385        390        395        400
Phe Thr Asn Tyr Asp Ile Tyr Lys Thr Leu Ser Lys Asp Ala Val Leu
  405        410        415
Leu Asp Ile Val Phe Pro Gly Tyr Thr Tyr Ile Phe Phe Gly Met Pro
  420        425        430
Glu Val Glu Phe Phe Met Val Asn Gln Leu Asn Asn Thr Arg Lys Thr
  435        440        445
Leu Lys Tyr Asn Pro Val Ser Lys Asp Ile Ile Ala Gly Thr Arg Asp
  450        455        460
Ser Glu Leu Glu Leu Pro Glu Thr Ser Asp Gln Pro Asn Tyr Glu
  465        470        475        480
Ser Tyr Ser His Arg Leu Cys His Ile Thr Ser Ile Pro Ala Thr Gly
  485        490        495
Ser Thr Thr Gly Leu Val Pro Val Phe Ser Trp Thr His Arg Ser Ala
  500        505        510
Asp Leu Ile Asn Ala Val His Ser Asp Lys Ile Thr Gln Ile Pro Val
  515        520        525
Val Lys Val Ser Asp Leu Ala Pro Ser Ile Thr Gly Gly Pro Asn Asn

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530 535 540
 Thr Val Val Ser Gly Pro Gly Phe Thr Gly Gly Gly Ile Ile Lys Val
 545 550 555 560
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 565 570 575
 Ile Asn Lys Glu Tyr Ser Met Arg Ile Arg Tyr Ala Ser Ala Asn Asn
 580 585 590
 Thr Glu Phe Tyr Ile Asn Pro Ser Glu Glu Asn Val Lys Ser His Ala
 595 600 605
 Gln Lys Thr Met Asn Arg Gly Glu Ala Leu Thr Tyr Asn Lys Phe Asn
 610 615 620
 Tyr Ala Thr Leu Pro Pro Ile Lys Phe Thr Thr Thr Glu Pro Phe Ile
 625 630 635 640
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 660 665

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 <211> 2010
 <212> DNA
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<220>
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<221> misc_feature
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 tcc acc tcc gtg tcc aac gac tcc aac cgc tac ccc ttc gcc aac gag 96
 Ser Thr Ser Val Ser Asn Asp Ser Asn Arg Tyr Pro Phe Ala Asn Glu
 20 25 30
 ccc acc aac gcc ctc cag aac atg gac tac aag gac tac ctc aag atg 144
 Pro Thr Asn Ala Leu Gln Asn Met Asp Tyr Lys Asp Tyr Leu Lys Met
 35 40 45
 tcc gcc ggc aac gcc tcc gag tac ccc ggc tcc ccc gag gtg ctc gtg 192
 Ser Ala Gly Asn Ala Ser Glu Tyr Pro Gly Ser Pro Glu Val Leu Val
 50 55 60
 tcc ggc cag gac gcc gcc aag gcc gcc atc gac atc gtg ggc aag ctc 240
 Ser Gly Gln Asp Ala Ala Lys Ala Ala Ile Asp Ile Val Gly Lys Leu
 65 70 75 80
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 Leu Ser Gly Leu Gly Val Pro Phe Val Gly Pro Ile Val Ser Leu Tyr
 85 90 95
 acc cag ctc atc gac atc ctc tgg ccc tcc ggc gag aag tcc cag tgg 336
 Thr Gln Leu Ile Asp Ile Leu Trp Pro Ser Gly Glu Lys Ser Gln Trp
 100 105 110

gaa atc ttc atg gag cag gtg gag gag ctc atc aac cag aag atc gcc	384
Glu Ile Phe Met Glu Gln Val Glu Leu Ile Asn Gln Lys Ile Ala	
115 120 125	
gag tac gcc cgc aac aag gcc ctc tcc gag ctg gag ggc ctc ggc aac	432
Glu Tyr Ala Arg Asn Lys Ala Leu Ser Glu Leu Glu Gly Leu Gly Asn	
130 135 140	
aac tac cag ctc tac ctc acc gcc ctg gag gag tgg gag gag aac ccc	480
Asn Tyr Gln Leu Tyr Leu Thr Ala Leu Glu Trp Glu Glu Asn Pro	
145 150 155 160	
aac ggc tcc cgc gcc ctc cgc gac gtg cgc aac cgc ttc gag atc ctc	528
Asn Gly Ser Arg Ala Leu Arg Asp Val Arg Asn Arg Phe Glu Ile Leu	
165 170 175	
gac tcc ctc ttc acc cag tac atg ccc tcc ttc cgc gtg acc aac ttc	576
Asp Ser Leu Phe Thr Gln Tyr Met Pro Ser Phe Arg Val Thr Asn Phe	
180 185 190	
gag gtg ccc ttc ctc acc gtg tac gcc atg gcc gcc aac ctc cac ctc	624
Glu Val Pro Phe Leu Thr Val Tyr Ala Met Ala Ala Asn Leu His Leu	
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ctc ctc ctc aag gac gcc tcc atc ttc ggc gag gag tgg ggc tgg tcc	672
Leu Leu Leu Lys Asp Ala Ser Ile Phe Gly Glu Glu Trp Gly Trp Ser	
210 215 220	
acc acc acc atc aac aac tac tac gac cgc cag atg aag ctc acc gcc	720
Thr Thr Thr Ile Asn Asn Tyr Tyr Asp Arg Gln Met Lys Leu Thr Ala	
225 230 235 240	
gag tac tcc gac cac tgc gtg aag tgg tat gag acc ggc ctc gcc aag	768
Glu Tyr Ser Asp His Cys Val Lys Trp Tyr Glu Thr Gly Leu Ala Lys	
245 250 255	
ctc aag ggc acc tcc gcc aag cag tgg gtg gac tac aac cag ttc cgc	816
Leu Lys Gly Thr Ser Ala Lys Gln Trp Val Asp Tyr Asn Gln Phe Arg	
260 265 270	
cgc gag atg acc ctc gcc gtg ctc gac gtg gtg gcc ctc ttc ccc aac	864
Arg Glu Met Thr Leu Ala Val Leu Asp Val Val Ala Leu Phe Pro Asn	
275 280 285	
tac gac acc cgc acc tac ccc atg gag acc aag gcc cag ctc acc cgc	912
Tyr Asp Thr Arg Thr Tyr Pro Met Glu Thr Lys Ala Gln Leu Thr Arg	
290 295 300	
gag gtg tac acc gac ccg ctc ggc gcc gtg aac gtg tcc tcc atc gcc	960
Glu Val Tyr Thr Asp Pro Leu Gly Ala Val Asn Val Ser Ser Ile Gly	
305 310 315 320	
tct tgg tac gac aag gcc cca agc ttc ggc gtg atc gag tcc tcc gtg	1008
Ser Trp Tyr Asp Lys Ala Pro Ser Phe Gly Val Ile Glu Ser Ser Val	
325 330 335	
atc cgc ccg ccg cac gtg ttc gac tac atc acc ggc ctc acc gtg tac	1056
Ile Arg Pro Pro His Val Phe Asp Tyr Ile Thr Gly Leu Thr Val Tyr	
340 345 350	
acc cag tcc cgc tcc atc tcc tcc gcc cgc tac atc cgc cac tgg gcc	1104
Thr Gln Ser Arg Ser Ile Ser Ser Ala Arg Tyr Ile Arg His Trp Ala	
355 360 365	

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Gly His Gln Ile Ser Tyr His Arg Val Ser Arg Gly Ser Asn Leu Gln	
370 375 380	
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Gln Met Tyr Gly Thr Asn Gln Asn Leu His Ser Thr Ser Thr Phe Asp	
385 390 395 400	
ttc acc aac tac gac atc tac aag acc ctc tcc aag gac gcc gtg ctc	1248
Phe Thr Asn Tyr Asp Ile Tyr Lys Thr Leu Ser Lys Asp Ala Val Leu	
405 410 415	
ctc gac atc gtg tac ccc ggc tac acc tac atc ttc ttc ggc atg ccg	1296
Leu Asp Ile Val Tyr Pro Gly Tyr Thr Tyr Ile Phe Phe Gly Met Pro	
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Glu Val Glu Phe Phe Met Val Asn Gln Leu Asn Asn Thr Arg Lys Thr	
435 440 445	
ctc aaa tac aac ccc gtg tcc aag gac atc atc gcc tcc acc cgc gac	1392
Leu Lys Tyr Asn Pro Val Ser Lys Asp Ile Ile Ala Ser Thr Arg Asp	
450 455 460	
tcc gag ctc gag ctc ccc ccc gag acc tcc gac cag ccc aac tac gag	1440
Ser Glu Leu Glu Leu Pro Pro Glu Thr Ser Asp Gln Pro Asn Tyr Glu	
465 470 475 480	
tcc tac tcc cac cgc ctc tgc cac atc acc tcc atc ccc gcc acc ggc	1488
Ser Tyr Ser His Arg Leu Cys His Ile Thr Ser Ile Pro Ala Thr Gly	
485 490 495	
aac acc acc ggc ctc gtg ccg gtg ttc tcc tgg acc cac cgc tct gca	1536
Asn Thr Thr Gly Leu Val Pro Val Phe Ser Trp Thr His Arg Ser Ala	
500 505 510	
gac ctc aac aac acc atc tac tcc gac aag atc acc cag atc ccc gcc	1584
Asp Leu Asn Asn Thr Ile Tyr Ser Asp Lys Ile Thr Gln Ile Pro Ala	
515 520 525	
gtg aag tgc tgg gac aac ctc ccc ttc gtg ccc gtg gtg aag ggc ccc	1632
Val Lys Cys Trp Asp Asn Leu Pro Phe Val Pro Val Val Lys Gly Pro	
530 535 540	
ggc cac acc ggc ggc gac ctc ctc cag tac aac cgc tcc acc ggc tcc	1680
Gly His Thr Gly Gly Asp Leu Leu Gln Tyr Asn Arg Ser Thr Gly Ser	
545 550 555 560	
gtg ggc acc ctc ttc ctc gcc cgc tac ggc ctc gcc ctg gag aag gcc	1728
Val Gly Thr Leu Phe Leu Ala Arg Tyr Gly Leu Ala Leu Glu Lys Ala	
565 570 575	
ggc aag tac cgc gtg cgc ctc cgc tac gcc act gac gcc gac atc gtg	1776
Gly Lys Tyr Arg Val Arg Leu Arg Tyr Ala Thr Asp Ala Asp Ile Val	
580 585 590	
ctc cac gtg aac gac gcc cag atc cag atg ccc aag acc atg aac ccc	1824
Leu His Val Asn Asp Ala Gln Ile Gln Met Pro Lys Thr Met Asn Pro	
595 600 605	
ggc gag gac ctc acc tcc aag acc ttc aag gtg gcc gac gcc atc acc	1872
Gly Glu Asp Leu Thr Ser Lys Thr Phe Lys Val Ala Asp Ala Ile Thr	

610	615	620	
acc ctc aac ctc gcc acc gac tcc tcc ctc gcc ctc aag cac aac ctc			1920
Thr Leu Asn Leu Ala Thr Asp Ser Ser Leu Ala Leu Lys His Asn Leu			
625	630	635	640
ggc gag gac ccc aac tcc acc ctc tcc ggc atc gtg tac gtg gac cgc			1968
Gly Glu Asp Pro Asn Ser Thr Leu Ser Gly Ile Val Tyr Val Asp Arg			
	645	650	655
atc gag ttc atc ccc gtg gac gag acc tac gag gcc gag tga			2010
Ile Glu Phe Ile Pro Val Asp Glu Thr Tyr Glu Ala Glu *			
	660	665	

<210> 10
 <211> 669
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Maize optimized Cry1218-1

<400> 10

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Ser	Thr	Ser	Val	Ser	Asn	Asp	Ser	Asn	Arg	Tyr	Pro	Phe	Ala	Asn	Glu
			20					25					30		
Pro	Thr	Asn	Ala	Leu	Gln	Asn	Met	Asp	Tyr	Lys	Asp	Tyr	Leu	Lys	Met
		35					40					45			
Ser	Ala	Gly	Asn	Ala	Ser	Glu	Tyr	Pro	Gly	Ser	Pro	Glu	Val	Leu	Val
	50					55					60				
Ser	Gly	Gln	Asp	Ala	Ala	Lys	Ala	Ala	Ile	Asp	Ile	Val	Gly	Lys	Leu
65				70					75					80	
Leu	Ser	Gly	Leu	Gly	Val	Pro	Phe	Val	Gly	Pro	Ile	Val	Ser	Leu	Tyr
				85					90					95	
Thr	Gln	Leu	Ile	Asp	Ile	Leu	Trp	Pro	Ser	Gly	Glu	Lys	Ser	Gln	Trp
		100						105						110	
Glu	Ile	Phe	Met	Glu	Gln	Val	Glu	Glu	Leu	Ile	Asn	Gln	Lys	Ile	Ala
		115					120					125			
Glu	Tyr	Ala	Arg	Asn	Lys	Ala	Leu	Ser	Glu	Leu	Glu	Gly	Leu	Gly	Asn
	130					135					140				
Asn	Tyr	Gln	Leu	Tyr	Leu	Thr	Ala	Leu	Glu	Glu	Trp	Glu	Glu	Asn	Pro
145					150					155					160
Asn	Gly	Ser	Arg	Ala	Leu	Arg	Asp	Val	Arg	Asn	Arg	Phe	Glu	Ile	Leu
				165					170					175	
Asp	Ser	Leu	Phe	Thr	Gln	Tyr	Met	Pro	Ser	Phe	Arg	Val	Thr	Asn	Phe
		180						185						190	
Glu	Val	Pro	Phe	Leu	Thr	Val	Tyr	Ala	Met	Ala	Ala	Asn	Leu	His	Leu
	195						200					205			
Leu	Leu	Leu	Lys	Asp	Ala	Ser	Ile	Phe	Gly	Glu	Glu	Trp	Gly	Trp	Ser
	210					215					220				
Thr	Thr	Thr	Ile	Asn	Asn	Tyr	Tyr	Asp	Arg	Gln	Met	Lys	Leu	Thr	Ala
225					230					235					240
Glu	Tyr	Ser	Asp	His	Cys	Val	Lys	Trp	Tyr	Glu	Thr	Gly	Leu	Ala	Lys
				245					250					255	
Leu	Lys	Gly	Thr	Ser	Ala	Lys	Gln	Trp	Val	Asp	Tyr	Asn	Gln	Phe	Arg
		260						265					270		
Arg	Glu	Met	Thr	Leu	Ala	Val	Leu	Asp	Val	Val	Ala	Leu	Phe	Pro	Asn
	275						280					285			
Tyr	Asp	Thr	Arg	Thr	Tyr	Pro	Met	Glu	Thr	Lys	Ala	Gln	Leu	Thr	Arg
	290					295					300				

Glu Val Tyr Thr Asp Pro Leu Gly Ala Val Asn Val Ser Ser Ile Gly
 305 310 315 320
 Ser Trp Tyr Asp Lys Ala Pro Ser Phe Gly Val Ile Glu Ser Ser Val
 325 330 335
 Ile Arg Pro Pro His Val Phe Asp Tyr Ile Thr Gly Leu Thr Val Tyr
 340 345 350
 Thr Gln Ser Arg Ser Ile Ser Ser Ala Arg Tyr Ile Arg His Trp Ala
 355 360 365
 Gly His Gln Ile Ser Tyr His Arg Val Ser Arg Gly Ser Asn Leu Gln
 370 375 380
 Gln Met Tyr Gly Thr Asn Gln Asn Leu His Ser Thr Ser Thr Phe Asp
 385 390 395 400
 Phe Thr Asn Tyr Asp Ile Tyr Lys Thr Leu Ser Lys Asp Ala Val Leu
 405 410 415
 Leu Asp Ile Val Tyr Pro Gly Tyr Thr Tyr Ile Phe Phe Gly Met Pro
 420 425 430
 Glu Val Glu Phe Phe Met Val Asn Gln Leu Asn Asn Thr Arg Lys Thr
 435 440 445
 Leu Lys Tyr Asn Pro Val Ser Lys Asp Ile Ile Ala Ser Thr Arg Asp
 450 455 460
 Ser Glu Leu Glu Leu Pro Pro Glu Thr Ser Asp Gln Pro Asn Tyr Glu
 465 470 475 480
 Ser Tyr Ser His Arg Leu Cys His Ile Thr Ser Ile Pro Ala Thr Gly
 485 490 495
 Asn Thr Thr Gly Leu Val Pro Val Phe Ser Trp Thr His Arg Ser Ala
 500 505 510
 Asp Leu Asn Asn Thr Ile Tyr Ser Asp Lys Ile Thr Gln Ile Pro Ala
 515 520 525
 Val Lys Cys Trp Asp Asn Leu Pro Phe Val Pro Val Val Lys Gly Pro
 530 535 540
 Gly His Thr Gly Gly Asp Leu Leu Gln Tyr Asn Arg Ser Thr Gly Ser
 545 550 555 560
 Val Gly Thr Leu Phe Leu Ala Arg Tyr Gly Leu Ala Leu Glu Lys Ala
 565 570 575
 Gly Lys Tyr Arg Val Arg Leu Arg Tyr Ala Thr Asp Ala Asp Ile Val
 580 585 590
 Leu His Val Asn Asp Ala Gln Ile Gln Met Pro Lys Thr Met Asn Pro
 595 600 605
 Gly Glu Asp Leu Thr Ser Lys Thr Phe Lys Val Ala Asp Ala Ile Thr
 610 615 620
 Thr Leu Asn Leu Ala Thr Asp Ser Ser Leu Ala Leu Lys His Asn Leu
 625 630 635 640
 Gly Glu Asp Pro Asn Ser Thr Leu Ser Gly Ile Val Tyr Val Asp Arg
 645 650 655
 Ile Glu Phe Ile Pro Val Asp Glu Thr Tyr Glu Ala Glu
 660 665

<210> 11
 <211> 2022
 <212> DNA
 <213> Bacillus thuringiensis (mutated)

<220>
 <221> CDS
 <222> (1)...(2022)
 <221> misc_feature
 <222> (0)...(0)
 <223> NGS.R.N1218-1

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1				5					10					15			
tct	act	tct	gta	tcc	aat	gat	tct	aac	aga	tac	cct	ttt	gcg	aat	gag	96	
Ser	Thr	Ser	Val	Ser	Asn	Asp	Ser	Asn	Arg	Tyr	Pro	Phe	Ala	Asn	Glu		
			20					25					30				
cca	aca	aat	gcg	cta	caa	aat	atg	gat	tat	aaa	gat	tat	tta	aaa	atg	144	
Pro	Thr	Asn	Ala	Leu	Gln	Asn	Met	Asp	Tyr	Lys	Asp	Tyr	Leu	Lys	Met		
		35					40					45					
tct	gcg	gga	aat	gct	agt	gaa	tac	cct	ggg	tca	cct	gaa	gta	ctt	gtt	192	
Ser	Ala	Gly	Asn	Ala	Ser	Glu	Tyr	Pro	Gly	Ser	Pro	Glu	Val	Leu	Val		
	50					55					60						
agc	gga	caa	gat	gca	gct	aag	gcc	gca	att	gat	ata	gta	ggg	aaa	tta	240	
Ser	Gly	Gln	Asp	Ala	Ala	Lys	Ala	Ala	Ile	Asp	Ile	Val	Gly	Lys	Leu		
	65					70				75					80		
cta	tca	ggg	tta	ggg	gtc	cca	ttt	gtt	ggg	ccg	ata	gtg	agt	ctt	tat	288	
Leu	Ser	Gly	Leu	Gly	Val	Pro	Phe	Val	Gly	Pro	Ile	Val	Ser	Leu	Tyr		
				85					90					95			
act	caa	ctt	att	gat	att	ctg	tgg	cct	tca	ggg	gaa	aag	agt	caa	tgg	336	
Thr	Gln	Leu	Ile	Asp	Ile	Leu	Trp	Pro	Ser	Gly	Glu	Lys	Ser	Gln	Trp		
			100					105					110				
gaa	att	ttt	atg	gaa	caa	gta	gaa	gaa	ctc	att	aat	caa	aaa	ata	gca	384	
Glu	Ile	Phe	Met	Glu	Gln	Val	Glu	Glu	Leu	Ile	Asn	Gln	Lys	Ile	Ala		
		115					120					125					
gaa	tat	gca	agg	aat	aaa	gcg	ctt	tcg	gaa	tta	gaa	gga	tta	ggg	aat	432	
Glu	Tyr	Ala	Arg	Asn	Lys	Ala	Leu	Ser	Glu	Leu	Glu	Gly	Leu	Gly	Asn		
		130				135						140					
aat	tac	caa	tta	tat	cta	act	gcg	ctt	gaa	gaa	tgg	gaa	gaa	aat	cca	480	
Asn	Tyr	Gln	Leu	Tyr	Leu	Thr	Ala	Leu	Glu	Glu	Trp	Glu	Glu	Asn	Pro		
					150						155				160		
aat	ggg	tca	aga	aat	ggg	tcc	cgg	gcc	tta	cga	gat	gtg	cga	aat	cga	528	
Asn	Gly	Ser	Arg	Asn	Gly	Ser	Arg	Ala	Leu	Arg	Asp	Val	Arg	Asn	Arg		
				165				170						175			
ttt	gaa	atc	ctg	gat	agt	tta	ttt	acg	caa	tat	atg	cca	tct	ttt	aga	576	
Phe	Glu	Ile	Leu	Asp	Ser	Leu	Phe	Thr	Gln	Tyr	Met	Pro	Ser	Phe	Arg		
			180					185					190				
gtg	aca	aat	ttt	gaa	gta	cca	ttc	ctt	act	gta	tat	gca	atg	gca	gcc	624	
Val	Thr	Asn	Phe	Glu	Val	Pro	Phe	Leu	Thr	Val	Tyr	Ala	Met	Ala	Ala		
		195					200					205					
aac	ctt	cat	tta	ctg	tta	tta	aag	gac	gcg	tca	att	ttt	gga	gaa	gaa	672	
Asn	Leu	His	Leu	Leu	Leu	Leu	Lys	Asp	Ala	Ser	Ile	Phe	Gly	Glu	Glu		
		210					215				220						
tgg	gga	tgg	tca	aca	act	act	att	aat	aac	tat	tat	gat	cgt	caa	atg	720	
Trp	Gly	Trp	Ser	Thr	Thr	Thr	Ile	Asn	Asn	Tyr	Tyr	Asp	Arg	Gln	Met		
		225				230				235					240		
aaa	ctt	act	gca	gaa	tat	tct	gat	cac	tgt	gta	aag	tgg	tat	gaa	act	768	
Lys	Leu	Thr	Ala	Glu	Tyr	Ser	Asp	His	Cys	Val	Lys	Trp	Tyr	Glu	Thr		
				245				250						255			

ggt tta gca aaa tta aaa ggc acg agc gct aaa caa tgg gtt gac tat 816
 Gly Leu Ala Lys Leu Lys Gly Thr Ser Ala Lys Gln Trp Val Asp Tyr
 260 265 270

aac caa ttc cgt aga gaa atg aca ctg gcg gtt tta gat gtt gtt gca 864
 Asn Gln Phe Arg Arg Glu Met Thr Leu Ala Val Leu Asp Val Val Ala
 275 280 285

tta ttc cca aat tat gac aca cgc acg tac cca atg gaa acg aaa gca 912
 Leu Phe Pro Asn Tyr Asp Thr Arg Thr Tyr Pro Met Glu Thr Lys Ala
 290 295 300

caa cta aca agg gaa gta tat aca gat cca ctg ggc gcg gta aac gtg 960
 Gln Leu Thr Arg Glu Val Tyr Thr Asp Pro Leu Gly Ala Val Asn Val
 305 310 315 320

tct tca att ggt tcc tgg tat gac aaa gca cct tct ttc gga gtg ata 1008
 Ser Ser Ile Gly Ser Trp Tyr Asp Lys Ala Pro Ser Phe Gly Val Ile
 325 330 335

gaa tca tcc gtt att cga cca ccc cat gta ttt gat tat ata acg gga 1056
 Glu Ser Ser Val Ile Arg Pro Pro His Val Phe Asp Tyr Ile Thr Gly
 340 345 350

ctc aca gtg tat aca caa tca aga agc att tct tcc gct cgc tat ata 1104
 Leu Thr Val Tyr Thr Gln Ser Arg Ser Ile Ser Ser Ala Arg Tyr Ile
 355 360 365

aga cat tgg gct ggt cat caa ata agc tac cat cgt gtc agt agg ggt 1152
 Arg His Trp Ala Gly His Gln Ile Ser Tyr His Arg Val Ser Arg Gly
 370 375 380

agt aat ctt caa caa atg tat gga act aat caa aat cta cac agc act 1200
 Ser Asn Leu Gln Gln Met Tyr Gly Thr Asn Gln Asn Leu His Ser Thr
 385 390 395 400

agt acc ttt gat ttt acg aat tat gat att tac aag act cta tca aag 1248
 Ser Thr Phe Asp Phe Thr Asn Tyr Asp Ile Tyr Lys Thr Leu Ser Lys
 405 410 415

gat gca gta ctc ctt gat att gtt tac cct ggt tat acg tat ata ttt 1296
 Asp Ala Val Leu Leu Asp Ile Val Tyr Pro Gly Tyr Thr Tyr Ile Phe
 420 425 430

ttt gga atg cca gaa gtc gag ttt ttc atg gta aac caa ttg aat aat 1344
 Phe Gly Met Pro Glu Val Glu Phe Phe Met Val Asn Gln Leu Asn Asn
 435 440 445

acc aga aag acg tta aag tat aat cca gtt tcc aaa gat att ata gcg 1392
 Thr Arg Lys Thr Leu Lys Tyr Asn Pro Val Ser Lys Asp Ile Ile Ala
 450 455 460

agt aca aga gat tcg gaa tta gaa tta cct cca gaa act tca gat caa 1440
 Ser Thr Arg Asp Ser Glu Leu Glu Leu Pro Pro Glu Thr Ser Asp Gln
 465 470 475 480

cca aat tat gag tca tat agc cat aga tta tgt cat atc aca agt att 1488
 Pro Asn Tyr Glu Ser Tyr Ser His Arg Leu Cys His Ile Thr Ser Ile
 485 490 495

ccc gcg acg ggt aac act acc gga tta gta cct gta ttt tct tgg aca 1536
 Pro Ala Thr Gly Asn Thr Thr Gly Leu Val Pro Val Phe Ser Trp Thr
 500 505 510

cat cga agt gca gat tta aac aat aca ata tat tca gat aaa atc act	1584
His Arg Ser Ala Asp Leu Asn Asn Thr Ile Tyr Ser Asp Lys Ile Thr	
515 520 525	
caa att ccg gcc gtt aaa tgt tgg gat aat tta ccg ttt gtt cca gtg	1632
Gln Ile Pro Ala Val Lys Cys Trp Asp Asn Leu Pro Phe Val Pro Val	
530 535 540	
gta aaa gga cca gga cat aca gga ggg gat tta tta cag tat aat aga	1680
Val Lys Gly Pro Gly His Thr Gly Gly Asp Leu Leu Gln Tyr Asn Arg	
545 550 555 560	
agt act ggt tct gta gga acc tta ttt cta gct cga tat ggc cta gca	1728
Ser Thr Gly Ser Val Gly Thr Leu Phe Leu Ala Arg Tyr Gly Leu Ala	
565 570 575	
tta gaa aaa gca ggg aaa tat cgt gta aga ctg aga tat gct act gat	1776
Leu Glu Lys Ala Gly Lys Tyr Arg Val Arg Leu Arg Tyr Ala Thr Asp	
580 585 590	
gca gat att gta ttg cat gta aac gat gct cag att cag atg cca aaa	1824
Ala Asp Ile Val Leu His Val Asn Asp Ala Gln Ile Gln Met Pro Lys	
595 600 605	
aca atg aac cca ggt gag gat ctg aca tct aaa act ttt aaa gtt gca	1872
Thr Met Asn Pro Gly Glu Asp Leu Thr Ser Lys Thr Phe Lys Val Ala	
610 615 620	
gat gct atc aca aca tta aat tta gca aca gat agt tcg cta gca ttg	1920
Asp Ala Ile Thr Thr Leu Asn Leu Ala Thr Asp Ser Ser Leu Ala Leu	
625 630 635 640	
aaa cat aat tta ggt gaa gac cct aat tca aca tta tct ggt ata gtt	1968
Lys His Asn Leu Gly Glu Asp Pro Asn Ser Thr Leu Ser Gly Ile Val	
645 650 655	
tac gtt gac cga atc gaa ttc atc cca gta gat gag aca tat gaa gcg	2016
Tyr Val Asp Arg Ile Glu Phe Ile Pro Val Asp Glu Thr Tyr Glu Ala	
660 665 670	
gaa taa	2022
Glu *	

<210> 12
 <211> 673
 <212> PRT
 <213> Bacillus thuringiensis (mutated)

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 Ser Thr Ser Val Ser Asn Asp Ser Asn Arg Tyr Pro Phe Ala Asn Glu
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 Pro Thr Asn Ala Leu Gln Asn Met Asp Tyr Lys Asp Tyr Leu Lys Met
 35 40 45
 Ser Ala Gly Asn Ala Ser Glu Tyr Pro Gly Ser Pro Glu Val Leu Val
 50 55 60
 Ser Gly Gln Asp Ala Ala Lys Ala Ala Ile Asp Ile Val Gly Lys Leu
 65 70 75 80
 Leu Ser Gly Leu Gly Val Pro Phe Val Gly Pro Ile Val Ser Leu Tyr

Ala Asp Ile Val Leu His Val Asn Asp Ala Gln Ile Gln Met Pro Lys
595 600 605
Thr Met Asn Pro Gly Glu Asp Leu Thr Ser Lys Thr Phe Lys Val Ala
610 615 620
Asp Ala Ile Thr Thr Leu Asn Leu Ala Thr Asp Ser Ser Leu Ala Leu
625 630 635 640
Lys His Asn Leu Gly Glu Asp Pro Asn Ser Thr Leu Ser Gly Ile Val
645 650 655
Tyr Val Asp Arg Ile Glu Phe Ile Pro Val Asp Glu Thr Tyr Glu Ala
660 665 670
Glu

<210> 13
<211> 12
<212> DNA
<213> Artificial Sequence

<220>

<223> NGSR Insert

<400> 13
aatggttccc gg

12

<210> 14
<211> 4
<212> PRT
<213> Artificial Sequence

<220>

<223> NGSR Insert

<400> 14
Asn Gly Ser Arg
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<210> 15
<211> 2010
<212> DNA
<213> Bacillus thuringiensis (truncated)

<220>

<221> CDS

<222> (1)...(2010)

<221> misc_feature

<222> (0)...(0)

<223> 1218-1A

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1 5 10 15

tct act tct gta tcc aat gat tct aac aga tac cct ttt gcg aat gag 96
Ser Thr Ser Val Ser Asn Asp Ser Asn Arg Tyr Pro Phe Ala Asn Glu
20 25 30

cca aca aat gcg cta caa aat atg gat tat aaa gat tat tta aaa atg 144
Pro Thr Asn Ala Leu Gln Asn Met Asp Tyr Lys Asp Tyr Leu Lys Met

35	40	45	
tct gcg gga aat gct agt gaa tac cct ggt tca cct gaa gta ctt gtt			192
Ser Ala Gly Asn Ala Ser Glu Tyr Pro Gly Ser Pro Glu Val Leu Val			
50	55	60	
agc gga caa gat gca gct aag gcc gca att gat ata gta ggt aaa tta			240
Ser Gly Gln Asp Ala Ala Lys Ala Ala Ile Asp Ile Val Gly Lys Leu			
65	70	75	80
cta tca ggt tta ggg gtc cca ttt gtt ggg ccg ata gtg agt ctt tat			288
Leu Ser Gly Leu Gly Val Pro Phe Val Gly Pro Ile Val Ser Leu Tyr			
	85	90	95
act caa ctt att gat att ctg tgg cct tca ggg gaa aag agt caa tgg			336
Thr Gln Leu Ile Asp Ile Leu Trp Pro Ser Gly Glu Lys Ser Gln Trp			
	100	105	110
gaa att ttt atg gaa caa gta gaa gaa ctc att aat caa aaa ata gca			384
Glu Ile Phe Met Glu Gln Val Glu Glu Leu Ile Asn Gln Lys Ile Ala			
	115	120	125
gaa tat gca agg aat aaa gcg ctt tcg gaa tta gaa gga tta ggt aat			432
Glu Tyr Ala Arg Asn Lys Ala Leu Ser Glu Leu Glu Gly Leu Gly Asn			
	130	135	140
aat tac caa tta tat cta act gcg ctt gaa gaa tgg gaa gaa aat cca			480
Asn Tyr Gln Leu Tyr Leu Thr Ala Leu Glu Glu Trp Glu Glu Asn Pro			
	145	150	155
aat ggt tca aga gcc tta cga gat gtg cga aat cga ttt gaa atc ctg			528
Asn Gly Ser Arg Ala Leu Arg Asp Val Arg Asn Arg Phe Glu Ile Leu			
	165	170	175
gat agt tta ttt acg caa tat atg cca tct ttt aga gtg aca aat ttt			576
Asp Ser Leu Phe Thr Gln Tyr Met Pro Ser Phe Arg Val Thr Asn Phe			
	180	185	190
gaa gta cca ttc ctt act gta tat gca atg gca gcc aac ctt cat tta			624
Glu Val Pro Phe Leu Thr Val Tyr Ala Met Ala Ala Asn Leu His Leu			
	195	200	205
ctg tta tta aag gac gcg tca att ttt gga gaa gaa tgg gga tgg tca			672
Leu Leu Leu Lys Asp Ala Ser Ile Phe Gly Glu Glu Trp Gly Trp Ser			
	210	215	220
aca act act att aat aac tat tat gat cgt caa atg aaa ctt act gca			720
Thr Thr Thr Ile Asn Asn Tyr Tyr Asp Arg Gln Met Lys Leu Thr Ala			
	225	230	235
gaa tat tct gat cac tgt gta aag tgg tat gaa act ggt tta gca aaa			768
Glu Tyr Ser Asp His Cys Val Lys Trp Tyr Glu Thr Gly Leu Ala Lys			
	245	250	255
tta aaa ggc acg agc gct aaa caa tgg gtt gac tat aac caa ttc cgt			816
Leu Lys Gly Thr Ser Ala Lys Gln Trp Val Asp Tyr Asn Gln Phe Arg			
	260	265	270
aga gaa atg aca ctg gcg gtt tta gat gtt gtt gca tta ttc cca aat			864
Arg Glu Met Thr Leu Ala Val Leu Asp Val Val Ala Leu Phe Pro Asn			
	275	280	285
tat gac aca cgc acg tac cca atg gaa acg aaa gca caa cta aca agg			912

Tyr	Asp	Thr	Arg	Thr	Tyr	Pro	Met	Glu	Thr	Lys	Ala	Gln	Leu	Thr	Arg		
290						295					300						
gaa	gta	tat	aca	gat	cca	ctg	ggc	gcg	gta	aac	gtg	tct	tca	att	ggg	960	
Glu	Val	Tyr	Thr	Asp	Pro	Leu	Gly	Ala	Val	Asn	Val	Ser	Ser	Ile	Gly		
305					310					315					320		
tcc	tgg	tat	gac	aaa	gca	cct	tct	ttc	gga	gtg	ata	gaa	tca	tcc	gtt	1008	
Ser	Trp	Tyr	Asp	Lys	Ala	Pro	Ser	Phe	Gly	Val	Ile	Glu	Ser	Ser	Val		
				325					330					335			
att	cga	cca	ccc	cat	gta	ttt	gat	tat	ata	acg	gga	ctc	aca	gtg	tat	1056	
Ile	Arg	Pro	Pro	His	Val	Phe	Asp	Tyr	Ile	Thr	Gly	Leu	Thr	Val	Tyr		
				340				345						350			
aca	caa	tca	aga	agc	att	tct	tcc	gct	cgc	tat	ata	aga	cat	tgg	gct	1104	
Thr	Gln	Ser	Arg	Ser	Ile	Ser	Ser	Ala	Arg	Tyr	Ile	Arg	His	Trp	Ala		
				355				360						365			
ggg	cat	caa	ata	agc	tac	cat	cgt	gtc	agt	agg	ggg	agt	aat	ctt	caa	1152	
Gly	His	Gln	Ile	Ser	Tyr	His	Arg	Val	Ser	Arg	Gly	Ser	Asn	Leu	Gln		
				370				375						380			
caa	atg	tat	gga	act	aat	caa	aat	cta	cac	agc	act	agt	acc	ttt	gat	1200	
Gln	Met	Tyr	Gly	Thr	Asn	Gln	Asn	Leu	His	Ser	Thr	Ser	Thr	Phe	Asp		
					390					395					400		
ttt	acg	aat	tat	gat	att	tac	aag	act	cta	tca	aag	gat	gca	gta	ctc	1248	
Phe	Thr	Asn	Tyr	Asp	Ile	Tyr	Lys	Thr	Leu	Ser	Lys	Asp	Ala	Val	Leu		
				405					410						415		
ctt	gat	att	gtt	tac	cct	ggg	tat	acg	tat	ata	ttt	ttt	gga	atg	cca	1296	
Leu	Asp	Ile	Val	Tyr	Pro	Gly	Tyr	Thr	Tyr	Ile	Phe	Phe	Gly	Met	Pro		
				420				425						430			
gaa	gtc	gag	ttt	ttc	atg	gta	aac	caa	ttg	aat	aat	acc	aga	aag	acg	1344	
Glu	Val	Glu	Phe	Phe	Met	Val	Asn	Gln	Leu	Asn	Asn	Thr	Arg	Lys	Thr		
			435				440						445				
tta	aag	tat	aat	cca	gtt	tcc	aaa	gat	att	ata	gcg	agt	aca	aga	gat	1392	
Leu	Lys	Tyr	Asn	Pro	Val	Ser	Lys	Asp	Ile	Ile	Ala	Ser	Thr	Arg	Asp		
					450		455				460						
tcg	gaa	tta	gaa	tta	cct	cca	gaa	act	tca	gat	caa	cca	aat	tat	gag	1440	
Ser	Glu	Leu	Glu	Leu	Pro	Pro	Glu	Thr	Ser	Asp	Gln	Pro	Asn	Tyr	Glu		
					470					475					480		
tca	tat	agc	cat	aga	tta	tgt	cat	atc	aca	agt	att	ccc	gcg	acg	ggg	1488	
Ser	Tyr	Ser	His	Arg	Leu	Cys	His	Ile	Thr	Ser	Ile	Pro	Ala	Thr	Gly		
				485					490					495			
aac	act	acc	gga	tta	gta	cct	gta	ttt	tct	tgg	aca	cat	cga	agt	gca	1536	
Asn	Thr	Thr	Gly	Leu	Val	Pro	Val	Phe	Ser	Trp	Thr	His	Arg	Ser	Ala		
			500					505					510				
gat	tta	aac	aat	aca	ata	tat	tca	gat	aaa	atc	act	caa	att	ccg	gcc	1584	
Asp	Leu	Asn	Asn	Thr	Ile	Tyr	Ser	Asp	Lys	Ile	Thr	Gln	Ile	Pro	Ala		
			515					520					525				
gtt	aaa	tgt	tgg	gat	aat	tta	ccg	ttt	gtt	cca	gtg	gta	aaa	gga	cca	1632	
Val	Lys	Cys	Trp	Asp	Asn	Leu	Pro	Phe	Val	Pro	Val	Val	Lys	Gly	Pro		
			530			535						540					

gga cat aca gga ggg gat tta tta cag tat aat aga agt act ggt tct 1680
 Gly His Thr Gly Gly Asp Leu Leu Gln Tyr Asn Arg Ser Thr Gly Ser
 545 550 555 560
 gta gga acc tta ttt cta gct cga tat ggc cta gca tta gaa aaa gca 1728
 Val Gly Thr Leu Phe Leu Ala Arg Tyr Gly Leu Ala Leu Glu Lys Ala
 565 570 575
 ggg aaa tat cgt gta aga ctg aga tat gct act gat gca gat att gta 1776
 Gly Lys Tyr Arg Val Arg Leu Arg Tyr Ala Thr Asp Ala Asp Ile Val
 580 585 590
 ttg cat gta aac gat gct cag att cag atg cca aaa aca atg aac cca 1824
 Leu His Val Asn Asp Ala Gln Ile Gln Met Pro Lys Thr Met Asn Pro
 595 600 605
 ggt gag gat ctg aca tct aaa act ttt aaa gtt gca gat gct atc aca 1872
 Gly Glu Asp Leu Thr Ser Lys Thr Phe Lys Val Ala Asp Ala Ile Thr
 610 615 620
 aca tta aat tta gca aca gat agt tcg cta gca ttg aaa cat aat tta 1920
 Thr Leu Asn Leu Ala Thr Asp Ser Ser Leu Ala Leu Lys His Asn Leu
 625 630 635 640
 ggt gaa gac cct aat tca aca tta tct ggt ata gtt tac gtt gac cga 1968
 Gly Glu Asp Pro Asn Ser Thr Leu Ser Gly Ile Val Tyr Val Asp Arg
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 atc gaa ttc atc cca gta gat gag aca tat gaa gcg gaa taa 2010
 Ile Glu Phe Ile Pro Val Asp Glu Thr Tyr Glu Ala Glu *
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 <213> Bacillus thuringiensis (truncated)

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 35 40 45
 Ser Ala Gly Asn Ala Ser Glu Tyr Pro Gly Ser Pro Glu Val Leu Val
 50 55 60
 Ser Gly Gln Asp Ala Ala Lys Ala Ala Ile Asp Ile Val Gly Lys Leu
 65 70 75 80
 Leu Ser Gly Leu Gly Val Pro Phe Val Gly Pro Ile Val Ser Leu Tyr
 85 90 95
 Thr Gln Leu Ile Asp Ile Leu Trp Pro Ser Gly Glu Lys Ser Gln Trp
 100 105 110
 Glu Ile Phe Met Glu Gln Val Glu Glu Leu Ile Asn Gln Lys Ile Ala
 115 120 125
 Glu Tyr Ala Arg Asn Lys Ala Leu Ser Glu Leu Glu Gly Leu Gly Asn
 130 135 140
 Asn Tyr Gln Leu Tyr Leu Thr Ala Leu Glu Glu Trp Glu Glu Asn Pro
 145 150 155 160
 Asn Gly Ser Arg Ala Leu Arg Asp Val Arg Asn Arg Phe Glu Ile Leu
 165 170 175
 Asp Ser Leu Phe Thr Gln Tyr Met Pro Ser Phe Arg Val Thr Asn Phe

			180					185					190			
Glu	Val	Pro	Phe	Leu	Thr	Val	Tyr	Ala	Met	Ala	Ala	Asn	Leu	His	Leu	
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Leu	Leu	Leu	Lys	Asp	Ala	Ser	Ile	Phe	Gly	Glu	Glu	Trp	Gly	Trp	Ser	
	210					215					220					
Thr	Thr	Thr	Ile	Asn	Asn	Tyr	Tyr	Asp	Arg	Gln	Met	Lys	Leu	Thr	Ala	
225					230					235					240	
Glu	Tyr	Ser	Asp	His	Cys	Val	Lys	Trp	Tyr	Glu	Thr	Gly	Leu	Ala	Lys	
				245					250					255		
Leu	Lys	Gly	Thr	Ser	Ala	Lys	Gln	Trp	Val	Asp	Tyr	Asn	Gln	Phe	Arg	
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Arg	Glu	Met	Thr	Leu	Ala	Val	Leu	Asp	Val	Val	Ala	Leu	Phe	Pro	Asn	
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Tyr	Asp	Thr	Arg	Thr	Tyr	Pro	Met	Glu	Thr	Lys	Ala	Gln	Leu	Thr	Arg	
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Glu	Val	Tyr	Thr	Asp	Pro	Leu	Gly	Ala	Val	Asn	Val	Ser	Ser	Ile	Gly	
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Ser	Trp	Tyr	Asp	Lys	Ala	Pro	Ser	Phe	Gly	Val	Ile	Glu	Ser	Ser	Val	
				325					330					335		
Ile	Arg	Pro	Pro	His	Val	Phe	Asp	Tyr	Ile	Thr	Gly	Leu	Thr	Val	Tyr	
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Thr	Gln	Ser	Arg	Ser	Ile	Ser	Ser	Ala	Arg	Tyr	Ile	Arg	His	Trp	Ala	
		355					360					365				
Gly	His	Gln	Ile	Ser	Tyr	His	Arg	Val	Ser	Arg	Gly	Ser	Asn	Leu	Gln	
	370					375					380					
Gln	Met	Tyr	Gly	Thr	Asn	Gln	Asn	Leu	His	Ser	Thr	Ser	Thr	Phe	Asp	
385					390					395					400	
Phe	Thr	Asn	Tyr	Asp	Ile	Tyr	Lys	Thr	Leu	Ser	Lys	Asp	Ala	Val	Leu	
			405						410					415		
Leu	Asp	Ile	Val	Tyr	Pro	Gly	Tyr	Thr	Tyr	Ile	Phe	Phe	Gly	Met	Pro	
			420					425					430			
Glu	Val	Glu	Phe	Phe	Met	Val	Asn	Gln	Leu	Asn	Asn	Thr	Arg	Lys	Thr	
		435					440					445				
Leu	Lys	Tyr	Asn	Pro	Val	Ser	Lys	Asp	Ile	Ile	Ala	Ser	Thr	Arg	Asp	
	450					455					460					
Ser	Glu	Leu	Glu	Leu	Pro	Pro	Glu	Thr	Ser	Asp	Gln	Pro	Asn	Tyr	Glu	
465					470					475					480	
Ser	Tyr	Ser	His	Arg	Leu	Cys	His	Ile	Thr	Ser	Ile	Pro	Ala	Thr	Gly	
			485						490					495		
Asn	Thr	Thr	Gly	Leu	Val	Pro	Val	Phe	Ser	Trp	Thr	His	Arg	Ser	Ala	
			500					505				510				
Asp	Leu	Asn	Asn	Thr	Ile	Tyr	Ser	Asp	Lys	Ile	Thr	Gln	Ile	Pro	Ala	
		515					520					525				
Val	Lys	Cys	Trp	Asp	Asn	Leu	Pro	Phe	Val	Pro	Val	Val	Lys	Gly	Pro	
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<221> misc_feature
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tct act tct gta tcc aat gat tct aac aga tac cct ttt gcg aat gag 96
Ser Thr Ser Val Ser Asn Asp Ser Asn Arg Tyr Pro Phe Ala Asn Glu
      20             25             30

cca aca aat gcg cta caa aat atg gat tat aaa gat tat tta aaa atg 144
Pro Thr Asn Ala Leu Gln Asn Met Asp Tyr Lys Asp Tyr Leu Lys Met
      35             40             45

tct gcg gga aat gct agt gaa tac cct ggt tca cct gaa gta ctt gtt 192
Ser Ala Gly Asn Ala Ser Glu Tyr Pro Gly Ser Pro Glu Val Leu Val
      50             55             60

agc gga caa gat gca gct aag gcc gca att gat ata gta ggt aaa tta 240
Ser Gly Gln Asp Ala Ala Lys Ala Ala Ile Asp Ile Val Gly Lys Leu
      65             70             75             80

cta tca ggt tta ggg gtc cca ttt gtt ggg ccg ata gtg agt ctt tat 288
Leu Ser Gly Leu Gly Val Pro Phe Val Gly Pro Ile Val Ser Leu Tyr
      85             90             95

act caa ctt att gat att ctg tgg cct tca ggg caa aag agt caa tgg 336
Thr Gln Leu Ile Asp Ile Leu Trp Pro Ser Gly Gln Lys Ser Gln Trp
      100            105            110

gag att ttt atg gaa caa gta gaa gaa ctc ata aat caa aaa ata gca 384
Glu Ile Phe Met Glu Gln Val Glu Glu Leu Ile Asn Gln Lys Ile Ala
      115            120            125

gaa tat gca agg aat aaa gcg ctt tcg gaa tta gaa gga tta ggt aat 432
Glu Tyr Ala Arg Asn Lys Ala Leu Ser Glu Leu Glu Gly Leu Gly Asn
      130            135            140

aat tac caa tta tat cta act gcg ctt gaa gaa tgg aaa gaa aat cca 480
Asn Tyr Gln Leu Tyr Leu Thr Ala Leu Glu Glu Trp Lys Glu Asn Pro
      145            150            155            160

aat ggt tca aga gcc tta cga gat gtg cga aat cga ttt gaa atc ctg 528
Asn Gly Ser Arg Ala Leu Arg Asp Val Arg Asn Arg Phe Glu Ile Leu
      165            170            175

gat agt tta ttt acg caa tac atg cca tct ttt cga gtg aca aat ttt 576
Asp Ser Leu Phe Thr Gln Tyr Met Pro Ser Phe Arg Val Thr Asn Phe
      180            185            190

gaa gta cca ttc ctt aca gta tat aca cag gca gcc aac ctt cat tta 624

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Glu Val Pro Phe Leu Thr Val Tyr Thr Gln Ala Ala Asn Leu His Leu	
195 200 205	
ctg tta tta aag gac gct tca att ttt gga gaa gaa tgg gga tgg tct	672
Leu Leu Leu Lys Asp Ala Ser Ile Phe Gly Glu Glu Trp Gly Trp Ser	
210 215 220	
aca acc act att aat aac tat tat gat cgt caa atg aaa ctt act gca	720
Thr Thr Thr Ile Asn Asn Tyr Tyr Asp Arg Gln Met Lys Leu Thr Ala	
225 230 235 240	
gaa tat tct gat cac tgt gta aag tgg tat gaa act ggt tta gca aaa	768
Glu Tyr Ser Asp His Cys Val Lys Trp Tyr Glu Thr Gly Leu Ala Lys	
245 250 255	
tta aaa ggc acg agc gct aaa caa tgg gtc gac tat aac caa ttc cgt	816
Leu Lys Gly Thr Ser Ala Lys Gln Trp Val Asp Tyr Asn Gln Phe Arg	
260 265 270	
aga gaa atg aca ctg acg gtt tta gat gtt gtt gca tta ttc cca aat	864
Arg Glu Met Thr Leu Thr Val Leu Asp Val Val Ala Leu Phe Pro Asn	
275 280 285	
tat gac aca cgc acg tac cca atg gaa acg aaa gca caa cta aca agg	912
Tyr Asp Thr Arg Thr Tyr Pro Met Glu Thr Lys Ala Gln Leu Thr Arg	
290 295 300	
gaa gta tat aca gat cca ctg ggc gcg gta aac gtg tct tca att ggt	960
Glu Val Tyr Thr Asp Pro Leu Gly Ala Val Asn Val Ser Ser Ile Gly	
305 310 315 320	
tcc tgg tat gac aaa gca cct tct ttc gga gtg ata gaa tca tcc gtt	1008
Ser Trp Tyr Asp Lys Ala Pro Ser Phe Gly Val Ile Glu Ser Ser Val	
325 330 335	
att cga cca ccc cat gta ttt gat tat ata acg gga ctc aca gtg tat	1056
Ile Arg Pro Pro His Val Phe Asp Tyr Ile Thr Gly Leu Thr Val Tyr	
340 345 350	
aca caa tca aga agc att tct tcc gct cgc tat ata aga cat tgg gct	1104
Thr Gln Ser Arg Ser Ile Ser Ser Ala Arg Tyr Ile Arg His Trp Ala	
355 360 365	
ggt cat caa ata agc tat cat cgg att ttt agt gat aat att ata aaa	1152
Gly His Gln Ile Ser Tyr His Arg Ile Phe Ser Asp Asn Ile Ile Lys	
370 375 380	
cag atg tat gga act aat caa aat cta cac agc act agt acc ttt gat	1200
Gln Met Tyr Gly Thr Asn Gln Asn Leu His Ser Thr Ser Thr Phe Asp	
385 390 395 400	
ttt acg aat tat gat att tac aag acg tta tca aaa gat gcg gtg ctc	1248
Phe Thr Asn Tyr Asp Ile Tyr Lys Thr Leu Ser Lys Asp Ala Val Leu	
405 410 415	
ctt gat att gtt ttt cct ggt tat acg tat ata ttt ttt gga atg cca	1296
Leu Asp Ile Val Phe Pro Gly Tyr Thr Tyr Ile Phe Phe Gly Met Pro	
420 425 430	
gaa gtc gag ttt ttc atg gta aac caa ttg aat aat acc aga aag acg	1344
Glu Val Glu Phe Phe Met Val Asn Gln Leu Asn Asn Thr Arg Lys Thr	
435 440 445	

tta aag tat aat ccg gtt tcc aaa gat att ata gcg ggg aca aga gat	1392
Leu Lys Tyr Asn Pro Val Ser Lys Asp Ile Ile Ala Gly Thr Arg Asp	
450 455 460	
tcg gaa tta gaa tta cct cca gaa act tca gat caa cca aat tat gag	1440
Ser Glu Leu Glu Leu Pro Pro Glu Thr Ser Asp Gln Pro Asn Tyr Glu	
465 470 475 480	
tca tat agc cat aga tta tgt cat atc aca agt att ccc gcg acg ggt	1488
Ser Tyr Ser His Arg Leu Cys His Ile Thr Ser Ile Pro Ala Thr Gly	
485 490 495	
tca act acc gga tta gta cct gta ttt tct tgg aca cat cgg agt gcc	1536
Ser Thr Thr Gly Leu Val Pro Val Phe Ser Trp Thr His Arg Ser Ala	
500 505 510	
gat ctt ata aat gca gtt cat tca gat aaa att act cag att ccg gtc	1584
Asp Leu Ile Asn Ala Val His Ser Asp Lys Ile Thr Gln Ile Pro Val	
515 520 525	
gta aag gtt tct gat ttg gct ccc tct ata aca gga ggg cca aat aat	1632
Val Lys Val Ser Asp Leu Ala Pro Ser Ile Thr Gly Gly Pro Asn Asn	
530 535 540	
acc gtt gta tcg ggt cct gga ttt aca ggg ggg ggg ata ata aaa gta	1680
Thr Val Val Ser Gly Pro Gly Phe Thr Gly Gly Gly Ile Ile Lys Val	
545 550 555 560	
ata aga aat gga gta att ata tca cat atg cgt gtt aaa att tca gac	1728
Ile Arg Asn Gly Val Ile Ile Ser His Met Arg Val Lys Ile Ser Asp	
565 570 575	
att aac aaa gaa tat agt atg agg att cgg tat gct tcc gct aat aat	1776
Ile Asn Lys Glu Tyr Ser Met Arg Ile Arg Tyr Ala Ser Ala Asn Asn	
580 585 590	
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Thr Glu Phe Tyr Ile Asn Pro Ser Glu Glu Asn Val Lys Ser His Ala	
595 600 605	
caa aaa act atg aat aga ggt gaa gct tta aca tat aat aaa ttt aat	1872
Gln Lys Thr Met Asn Arg Gly Glu Ala Leu Thr Tyr Asn Lys Phe Asn	
610 615 620	
tat gcg act ttg ccc cct att aaa ttt acg aca acc gaa cct ttc att	1920
Tyr Ala Thr Leu Pro Pro Ile Lys Phe Thr Thr Thr Glu Pro Phe Ile	
625 630 635 640	
act cta ggg gct ata ttt gaa gcg gaa gac ttt ctt gga att gaa gct	1968
Thr Leu Gly Ala Ile Phe Glu Ala Glu Asp Phe Leu Gly Ile Glu Ala	
645 650 655	
tat ata gac cga atc gaa ttt atc cca gta gat gag aca tat gaa gcg	2016
Tyr Ile Asp Arg Ile Glu Phe Ile Pro Val Asp Glu Thr Tyr Glu Ala	
660 665 670	
gaa taa	2022
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<212> PRT

<213> *Bacillus thuringiensis* (truncated)

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35 40 45
Ser Ala Gly Asn Ala Ser Glu Tyr Pro Gly Ser Pro Glu Val Leu Val
50 55 60
Ser Gly Gln Asp Ala Ala Lys Ala Ala Ile Asp Ile Val Gly Lys Leu
65 70 75 80
Leu Ser Gly Leu Gly Val Pro Phe Val Gly Pro Ile Val Ser Leu Tyr
85 90 95
Thr Gln Leu Ile Asp Ile Leu Trp Pro Ser Gly Gln Lys Ser Gln Trp
100 105 110
Glu Ile Phe Met Glu Gln Val Glu Glu Leu Ile Asn Gln Lys Ile Ala
115 120 125
Glu Tyr Ala Arg Asn Lys Ala Leu Ser Glu Leu Glu Gly Leu Gly Asn
130 135 140
Asn Tyr Gln Leu Tyr Leu Thr Ala Leu Glu Glu Trp Lys Glu Asn Pro
145 150 155 160
Asn Gly Ser Arg Ala Leu Arg Asp Val Arg Asn Arg Phe Glu Ile Leu
165 170 175
Asp Ser Leu Phe Thr Gln Tyr Met Pro Ser Phe Arg Val Thr Asn Phe
180 185 190
Glu Val Pro Phe Leu Thr Val Tyr Thr Gln Ala Ala Asn Leu His Leu
195 200 205
Leu Leu Leu Lys Asp Ala Ser Ile Phe Gly Glu Glu Trp Gly Trp Ser
210 215 220
Thr Thr Thr Ile Asn Asn Tyr Tyr Asp Arg Gln Met Lys Leu Thr Ala
225 230 235 240
Glu Tyr Ser Asp His Cys Val Lys Trp Tyr Glu Thr Gly Leu Ala Lys
245 250 255
Leu Lys Gly Thr Ser Ala Lys Gln Trp Val Asp Tyr Asn Gln Phe Arg
260 265 270
Arg Glu Met Thr Leu Thr Val Leu Asp Val Val Ala Leu Phe Pro Asn
275 280 285
Tyr Asp Thr Arg Thr Tyr Pro Met Glu Thr Lys Ala Gln Leu Thr Arg
290 295 300
Glu Val Tyr Thr Asp Pro Leu Gly Ala Val Asn Val Ser Ser Ile Gly
305 310 315 320
Ser Trp Tyr Asp Lys Ala Pro Ser Phe Gly Val Ile Glu Ser Ser Val
325 330 335
Ile Arg Pro Pro His Val Phe Asp Tyr Ile Thr Gly Leu Thr Val Tyr
340 345 350
Thr Gln Ser Arg Ser Ile Ser Ser Ala Arg Tyr Ile Arg His Trp Ala
355 360 365
Gly His Gln Ile Ser Tyr His Arg Ile Phe Ser Asp Asn Ile Ile Lys
370 375 380
Gln Met Tyr Gly Thr Asn Gln Asn Leu His Ser Thr Ser Thr Phe Asp
385 390 395 400
Phe Thr Asn Tyr Asp Ile Tyr Lys Thr Leu Ser Lys Asp Ala Val Leu
405 410 415
Leu Asp Ile Val Phe Pro Gly Tyr Thr Tyr Ile Phe Phe Gly Met Pro
420 425 430
Glu Val Glu Phe Phe Met Val Asn Gln Leu Asn Asn Thr Arg Lys Thr
435 440 445
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Ser Glu Leu Glu Leu Pro Pro Glu Thr Ser Asp Gln Pro Asn Tyr Glu

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agt ctt tat act caa ctt att gat att ctg tgg cct tca ggg gaa aag 195
 Ser Leu Tyr Thr Gln Leu Ile Asp Ile Leu Trp Pro Ser Gly Glu Lys
 50 55 60

43

aaa ata gca gaa tat gca agg aat aaa gcg ctt tcg gaa tta gaa gga	291
Lys Ile Ala Glu Tyr Ala Arg Asn Lys Ala Leu Ser Glu Leu Glu Gly	
80 85 90	
tta ggt aat aat tac caa tta tat cta act gcg ctt gaa gaa tgg gaa	339
Leu Gly Asn Asn Tyr Gln Leu Tyr Leu Thr Ala Leu Glu Glu Trp Glu	
95 100 105 110	
gaa aat cca aat ggt tca aga gcc tta cga gat gtg cga aat cga ttt	387
Glu Asn Pro Asn Gly Ser Arg Ala Leu Arg Asp Val Arg Asn Arg Phe	
115 120 125	
gaa atc ctg gat agt tta ttt acg caa tat atg cca tct ttt aga gtg	435
Glu Ile Leu Asp Ser Leu Phe Thr Gln Tyr Met Pro Ser Phe Arg Val	
130 135 140	
aca aat ttt gaa gta cca ttc ctt act gta tat gca atg gca gcc aac	483
Thr Asn Phe Glu Val Pro Phe Leu Thr Val Tyr Ala Met Ala Ala Asn	
145 150 155	
ctt cat tta ctg tta tta aag gac gcg tca att ttt gga gaa gaa tgg	531
Leu His Leu Leu Leu Leu Lys Asp Ala Ser Ile Phe Gly Glu Glu Trp	
160 165 170	
gga tgg tca aca act act att aat aac tat tat gat cgt caa atg aaa	579
Gly Trp Ser Thr Thr Thr Ile Asn Asn Tyr Tyr Asp Arg Gln Met Lys	
175 180 185 190	
ctt act gca gaa tat tct gat cac tgt gta aag tgg tat gaa act ggt	627
Leu Thr Ala Glu Tyr Ser Asp His Cys Val Lys Trp Tyr Glu Thr Gly	
195 200 205	
tta gca aaa tta aaa ggc acg agc gct aaa caa tgg gtt gac tat aac	675
Leu Ala Lys Leu Lys Gly Thr Ser Ala Lys Gln Trp Val Asp Tyr Asn	
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Gln Phe Arg Arg Glu Met Thr Leu Ala Val Leu Asp Val Val Ala Leu	
225 230 235	
ttc cca aat tat gac aca cgc acg tac cca atg gaa acg aaa gca caa	771
Phe Pro Asn Tyr Asp Thr Arg Thr Tyr Pro Met Glu Thr Lys Ala Gln	
240 245 250	
cta aca agg gaa gta tat aca gat cca ctg ggc gcg gta aac gtg tct	819
Leu Thr Arg Glu Val Tyr Thr Asp Pro Leu Gly Ala Val Asn Val Ser	
255 260 265 270	
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Ser Ile Gly Ser Trp Tyr Asp Lys Ala Pro Ser Phe Gly Val Ile Glu	
275 280 285	
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Ser Ser Val Ile Arg Pro Pro His Val Phe Asp Tyr Ile Thr Gly Leu	
290 295 300	
aca gtg tat aca caa tca aga agc att tct tcc gct cgc tat ata aga	963
Thr Val Tyr Thr Gln Ser Arg Ser Ile Ser Ser Ala Arg Tyr Ile Arg	
305 310 315	
cat tgg gct ggt cat caa ata agc tac cat cgt gtc agt agg ggt agt	1011
His Trp Ala Gly His Gln Ile Ser Tyr His Arg Val Ser Arg Gly Ser	
320 325 330	

aat ctt caa caa atg tat gga act aat caa aat cta cac agc act agt	1059
Asn Leu Gln Gln Met Tyr Gly Thr Asn Gln Asn Leu His Ser Thr Ser	
335 340 345 350	
acc ttt gat ttt acg aat tat gat att tac aag act cta tca aag gat	1107
Thr Phe Asp Phe Thr Asn Tyr Asp Ile Tyr Lys Thr Leu Ser Lys Asp	
355 360 365	
gca gta ctc ctt gat att gtt tac cct ggt tat acg tat ata ttt ttt	1155
Ala Val Leu Leu Asp Ile Val Tyr Pro Gly Tyr Thr Tyr Ile Phe Phe	
370 375 380	
gga atg cca gaa gtc gag ttt ttc atg gta aac caa ttg aat aat acc	1203
Gly Met Pro Glu Val Glu Phe Phe Met Val Asn Gln Leu Asn Asn Thr	
385 390 395	
aga aag acg tta aag tat aat cca gtt tcc aaa gat att ata gcg agt	1251
Arg Lys Thr Leu Lys Tyr Asn Pro Val Ser Lys Asp Ile Ile Ala Ser	
400 405 410	
aca aga gat tcg gaa tta gaa tta cct cca gaa act tca gat caa cca	1299
Thr Arg Asp Ser Glu Leu Glu Leu Pro Pro Glu Thr Ser Asp Gln Pro	
415 420 425 430	
aat tat gag tca tat agc cat aga tta tgt cat atc aca agt att ccc	1347
Asn Tyr Glu Ser Tyr Ser His Arg Leu Cys His Ile Thr Ser Ile Pro	
435 440 445	
gcg acg ggt aac act acc gga tta gta cct gta ttt tct tgg aca cat	1395
Ala Thr Gly Asn Thr Thr Gly Leu Val Pro Val Phe Ser Trp Thr His	
450 455 460	
cga agt gca gat tta aac aat aca ata tat tca gat aaa atc act caa	1443
Arg Ser Ala Asp Leu Asn Asn Thr Ile Tyr Ser Asp Lys Ile Thr Gln	
465 470 475	
att ccg gcc gtt aaa tgt tgg gat aat tta ccg ttt gtt cca gtg gta	1491
Ile Pro Ala Val Lys Cys Trp Asp Asn Leu Pro Phe Val Pro Val Val	
480 485 490	
aaa gga cca gga cat aca gga ggg gat tta tta cag tat aat aga agt	1539
Lys Gly Pro Gly His Thr Gly Gly Asp Leu Leu Gln Tyr Asn Arg Ser	
495 500 505 510	
act ggt tct gta gga acc tta ttt cta gct cga tat ggc cta gca tta	1587
Thr Gly Ser Val Gly Thr Leu Phe Leu Ala Arg Tyr Gly Leu Ala Leu	
515 520 525	
gaa aaa gca ggg aaa tat cgt gta aga ctg aga tat gct act gat gca	1635
Glu Lys Ala Gly Lys Tyr Arg Val Arg Leu Arg Tyr Ala Thr Asp Ala	
530 535 540	
gat att gta ttg cat gta aac gat gct cag att cag atg cca aaa aca	1683
Asp Ile Val Leu His Val Asn Asp Ala Gln Ile Gln Met Pro Lys Thr	
545 550 555	
atg aac cca ggt gag gat ctg aca tct aaa act ttt aaa gtt gca gat	1731
Met Asn Pro Gly Glu Asp Leu Thr Ser Lys Thr Phe Lys Val Ala Asp	
560 565 570	
gct atc aca aca tta aat tta gca aca gat agt tcg cta gca ttg aaa	1779
Ala Ile Thr Thr Leu Asn Leu Ala Thr Asp Ser Ser Leu Ala Leu Lys	

The figure consists of ten horizontal gel electrophoresis panels, each containing multiple lanes of DNA bands. The panels are arranged vertically and labeled as follows:

- A**: Shows several lanes with distinct banding patterns.
- B**: Similar to A, with clear band separation.
- C**: Displays a different set of banding patterns.
- D**: Another panel showing unique DNA profiles.
- E**: Continues the sequence of DNA analysis.
- F**: Shows bands across its respective lanes.
- G**: Another gel panel in the series.
- H**: Displays DNA banding results.
- I**: Shows another set of DNA profiles.
- J**: The final panel in the figure, showing DNA bands.

Each panel typically has approximately 8-10 lanes, though some have fewer or more. The bands vary in intensity and position across the different panels, indicating different genetic or molecular states.

```

Leu Leu Asp Ile Val Tyr Pro Gly Tyr Thr Tyr Ile Phe Phe Gly Met
 370          375          380
Pro Glu Val Glu Phe Phe Met Val Asn Gln Leu Asn Asn Thr Arg Lys
385          390          395          400
Thr Leu Lys Tyr Asn Pro Val Ser Lys Asp Ile Ile Ala Ser Thr Arg
          405          410          415
Asp Ser Glu Leu Glu Leu Pro Pro Glu Thr Ser Asp Gln Pro Asn Tyr
          420          425          430
Glu Ser Tyr Ser His Arg Leu Cys His Ile Thr Ser Ile Pro Ala Thr
          435          440          445
Gly Asn Thr Thr Gly Leu Val Pro Val Phe Ser Trp Thr His Arg Ser
          450          455          460
Ala Asp Leu Asn Asn Thr Ile Tyr Ser Asp Lys Ile Thr Gln Ile Pro
465          470          475          480
Ala Val Lys Cys Trp Asp Asn Leu Pro Phe Val Pro Val Val Lys Gly
          485          490          495
Pro Gly His Thr Gly Gly Asp Leu Leu Gln Tyr Asn Arg Ser Thr Gly
          500          505          510
Ser Val Gly Thr Leu Phe Leu Ala Arg Tyr Gly Leu Ala Leu Glu Lys
          515          520          525
Ala Gly Lys Tyr Arg Val Arg Leu Arg Tyr Ala Thr Asp Ala Asp Ile
          530          535          540
Val Leu His Val Asn Asp Ala Gln Ile Gln Met Pro Lys Thr Met Asn
545          550          555          560
Pro Gly Glu Asp Leu Thr Ser Lys Thr Phe Lys Val Ala Asp Ala Ile
          565          570          575
Thr Thr Leu Asn Leu Ala Thr Asp Ser Ser Leu Ala Leu Lys His Asn
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Leu Gly Glu Asp Pro Asn Ser Thr Leu Ser Gly Ile Val Tyr Val Asp
          595          600          605
Arg Ile Glu Phe Ile Pro Val Asp
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<210> 21
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 <212> DNA
 <213> Bacillus thuringiensis (mutated)

<220>
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tct act tct gta tcc aat gat tct aac aga tac cct ttt gcg aat gag 96
Ser Thr Ser Val Ser Asn Asp Ser Asn Arg Tyr Pro Phe Ala Asn Glu
          20          25          30

cca aca aat gcg cta caa aat atg gat tat aaa gat tat tta aaa atg 144
Pro Thr Asn Ala Leu Gln Asn Met Asp Tyr Lys Asp Tyr Leu Lys Met
          35          40          45

tct gcg gga aat gct agt gaa tac cct ggt tca cct gaa gta ctt gtt 192
Ser Ala Gly Asn Ala Ser Glu Tyr Pro Gly Ser Pro Glu Val Leu Val
          50          55          60

```

agc gga caa gat gca gct aag gcc gca att gat ata gta ggt aaa tta	240
Ser Gly Gln Asp Ala Ala Lys Ala Ala Ile Asp Ile Val Gly Lys Leu	
65 70 75 80	
cta tca ggt tta ggg gtc cca ttt gtt ggg ccg ata gtg agt ctt tat	288
Leu Ser Gly Leu Gly Val Pro Phe Val Gly Pro Ile Val Ser Leu Tyr	
85 90 95	
act caa ctt att gat att ctg tgg cct tca ggg gaa aag agt caa tgg	336
Thr Gln Leu Ile Asp Ile Leu Trp Pro Ser Gly Glu Lys Ser Gln Trp	
100 105 110	
gaa att ttt atg gaa caa gta gaa gaa ctc att aat caa aaa ata gca	384
Glu Ile Phe Met Glu Gln Val Glu Glu Leu Ile Asn Gln Lys Ile Ala	
115 120 125	
gaa tat gca agg aat aaa gcg ctt tcg gaa tta gaa gga tta ggt aat	432
Glu Tyr Ala Arg Asn Lys Ala Leu Ser Glu Leu Glu Gly Leu Gly Asn	
130 135 140	
aat tac caa tta tat cta act gcg ctt gaa gaa tgg gaa gaa aat cca	480
Asn Tyr Gln Leu Tyr Leu Thr Ala Leu Glu Glu Trp Glu Glu Asn Pro	
145 150 155 160	
tta aaa atg tct aat ggt tca aga gcc tta cga gat gtg cga aat cga	528
Leu Lys Met Ser Asn Gly Ser Arg Ala Leu Arg Asp Val Arg Asn Arg	
165 170 175	
ttt gaa atc ctg gat agt tta ttt acg caa tat atg cca tct ttt aga	576
Phe Glu Ile Leu Asp Ser Leu Phe Thr Gln Tyr Met Pro Ser Phe Arg	
180 185 190	
gtg aca aat ttt gaa gta cca ttc ctt act gta tat gca atg gca gcc	624
Val Thr Asn Phe Glu Val Pro Phe Leu Thr Val Tyr Ala Met Ala Ala	
195 200 205	
aac ctt cat tta ctg tta tta aag gac gcg tca att ttt gga gaa gaa	672
Asn Leu His Leu Leu Leu Leu Lys Asp Ala Ser Ile Phe Gly Glu Glu	
210 215 220	
tgg gga tgg tca aca act act att aat aac tat tat gat cgt caa atg	720
Trp Gly Trp Ser Thr Thr Thr Ile Asn Asn Tyr Tyr Asp Arg Gln Met	
225 230 235 240	
aaa ctt act gca gaa tat tct gat cac tgt gta aag tgg tat gaa act	768
Lys Leu Thr Ala Glu Tyr Ser Asp His Cys Val Lys Trp Tyr Glu Thr	
245 250 255	
ggg tta gca aaa tta aaa ggc acg agc gct aaa caa tgg gtt gac tat	816
Gly Leu Ala Lys Leu Lys Gly Thr Ser Ala Lys Gln Trp Val Asp Tyr	
260 265 270	
aac caa ttc cgt aga gaa atg aca ctg gcg gtt tta gat gtt gtt gca	864
Asn Gln Phe Arg Arg Glu Met Thr Leu Ala Val Leu Asp Val Val Ala	
275 280 285	
tta ttc cca aat tat gac aca cgc acg tac cca atg gaa acg aaa gca	912
Leu Phe Pro Asn Tyr Asp Thr Arg Thr Tyr Pro Met Glu Thr Lys Ala	
290 295 300	
caa cta aca agg gaa gta tat aca gat cca ctg ggc gcg gta aac gtg	960
Gln Leu Thr Arg Glu Val Tyr Thr Asp Pro Leu Gly Ala Val Asn Val	

305	310	315	320	
tct tca att ggt tcc tgg tat gac aaa gca cct tct ttc gga gtg ata				1008
Ser Ser Ile Gly Ser Trp Tyr Asp Lys Ala Pro Ser Phe Gly Val Ile	325	330	335	
gaa tca tcc gtt att cga cca ccc cat gta ttt gat tat ata acg gga				1056
Glu Ser Ser Val Ile Arg Pro Pro His Val Phe Asp Tyr Ile Thr Gly	340	345	350	
ctc aca gtg tat aca caa tca aga agc att tct tcc gct cgc tat ata				1104
Leu Thr Val Tyr Thr Gln Ser Arg Ser Ile Ser Ser Ala Arg Tyr Ile	355	360	365	
aga cat tgg gct ggt cat caa ata agc tac cat cgt gtc agt agg ggt				1152
Arg His Trp Ala Gly His Gln Ile Ser Tyr His Arg Val Ser Arg Gly	370	375	380	
agt aat ctt caa caa atg tat gga act aat caa aat cta cac agc act				1200
Ser Asn Leu Gln Gln Met Tyr Gly Thr Asn Gln Asn Leu His Ser Thr	385	390	395	400
agt acc ttt gat ttt acg aat tat gat att tac aag act cta tca aag				1248
Ser Thr Phe Asp Phe Thr Asn Tyr Asp Ile Tyr Lys Thr Leu Ser Lys	405	410	415	
gat gca gta ctc ctt gat att gtt tac cct ggt tat acg tat ata ttt				1296
Asp Ala Val Leu Leu Asp Ile Val Tyr Pro Gly Tyr Thr Tyr Ile Phe	420	425	430	
ttt gga atg cca gaa gtc gag ttt ttc atg gta aac caa ttg aat aat				1344
Phe Gly Met Pro Glu Val Glu Phe Phe Met Val Asn Gln Leu Asn Asn	435	440	445	
acc aga aag acg tta aag tat aat cca gtt tcc aaa gat att ata gcg				1392
Thr Arg Lys Thr Leu Lys Tyr Asn Pro Val Ser Lys Asp Ile Ile Ala	450	455	460	
agt aca aga gat tcg gaa tta gaa tta cct cca gaa act tca gat caa				1440
Ser Thr Arg Asp Ser Glu Leu Glu Leu Pro Pro Glu Thr Ser Asp Gln	465	470	475	480
cca aat tat gag tca tat agc cat aga tta tgt cat atc aca agt att				1488
Pro Asn Tyr Glu Ser Tyr Ser His Arg Leu Cys His Ile Thr Ser Ile	485	490	495	
ccc gcg acg ggt aac act acc gga tta gta cct gta ttt tct tgg aca				1536
Pro Ala Thr Gly Asn Thr Thr Gly Leu Val Pro Val Phe Ser Trp Thr	500	505	510	
cat cga agt gca gat tta aac aat aca ata tat tca gat aaa atc act				1584
His Arg Ser Ala Asp Leu Asn Asn Thr Ile Tyr Ser Asp Lys Ile Thr	515	520	525	
caa att ccg gcc gtt aaa tgt tgg gat aat tta ccg ttt gtt cca gtg				1632
Gln Ile Pro Ala Val Lys Cys Trp Asp Asn Leu Pro Phe Val Pro Val	530	535	540	
gta aaa gga cca gga cat aca gga ggg gat tta tta cag tat aat aga				1680
Val Lys Gly Pro Gly His Thr Gly Gly Asp Leu Leu Gln Tyr Asn Arg	545	550	555	560
agt act ggt tct gta gga acc tta ttt cta gct cga tat ggc cta gca				1728

Ser Thr Gly Ser Val Gly Thr Leu Phe Leu Ala Arg Tyr Gly Leu Ala	
565 570 575	
tta gaa aaa gca ggg aaa tat cgt gta aga ctg aga tat gct act gat	1776
Leu Glu Lys Ala Gly Lys Tyr Arg Val Arg Leu Arg Tyr Ala Thr Asp	
580 585 590	
gca gat att gta ttg cat gta aac gat gct cag att cag atg cca aaa	1824
Ala Asp Ile Val Leu His Val Asn Asp Ala Gln Ile Gln Met Pro Lys	
595 600 605	
aca atg aac cca ggt gag gat ctg aca tct aaa act ttt aaa gtt gca	1872
Thr Met Asn Pro Gly Glu Asp Leu Thr Ser Lys Thr Phe Lys Val Ala	
610 615 620	
gat gct atc aca aca tta aat tta gca aca gat agt tcg cta gca ttg	1920
Asp Ala Ile Thr Thr Leu Asn Leu Ala Thr Asp Ser Ser Leu Ala Leu	
625 630 635 640	
aaa cat aat tta ggt gaa gac cct aat tca aca tta tct ggt ata gtt	1968
Lys His Asn Leu Gly Glu Asp Pro Asn Ser Thr Leu Ser Gly Ile Val	
645 650 655	
tac gtt gac cga atc gaa ttc atc cca gta gat gag aca tat gaa gcg	2016
Tyr Val Asp Arg Ile Glu Phe Ile Pro Val Asp Glu Thr Tyr Glu Ala	
660 665 670	
gaa taa	2022
Glu *	

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Pro Thr Asn Ala Leu Gln Asn Met Asp Tyr Lys Asp Tyr Leu Lys Met	
35 40 45	
Ser Ala Gly Asn Ala Ser Glu Tyr Pro Gly Ser Pro Glu Val Leu Val	
50 55 60	
Ser Gly Gln Asp Ala Ala Lys Ala Ala Ile Asp Ile Val Gly Lys Leu	
65 70 75 80	
Leu Ser Gly Leu Gly Val Pro Phe Val Gly Pro Ile Val Ser Leu Tyr	
85 90 95	
Thr Gln Leu Ile Asp Ile Leu Trp Pro Ser Gly Glu Lys Ser Gln Trp	
100 105 110	
Glu Ile Phe Met Glu Gln Val Glu Leu Ile Asn Gln Lys Ile Ala	
115 120 125	
Glu Tyr Ala Arg Asn Lys Ala Leu Ser Glu Leu Glu Gly Leu Gly Asn	
130 135 140	
Asn Tyr Gln Leu Tyr Leu Thr Ala Leu Glu Glu Trp Glu Glu Asn Pro	
145 150 155 160	
Leu Lys Met Ser Asn Gly Ser Arg Ala Leu Arg Asp Val Arg Asn Arg	
165 170 175	
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<210> 23
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 tct act tct gta tcc aat gat tct aac aga tac cct ttt gcg aat gag 96
 Ser Thr Ser Val Ser Asn Asp Ser Asn Arg Tyr Pro Phe Ala Asn Glu
 20 25 30
 cca aca aat gcg cta caa aat atg gat tat aaa gat tat tta aaa atg 144
 Pro Thr Asn Ala Leu Gln Asn Met Asp Tyr Lys Asp Tyr Leu Lys Met
 35 40 45
 tct gcg gga aat gct agt gaa tac cct ggt tca cct gaa gta ctt gtt 192
 Ser Ala Gly Asn Ala Ser Glu Tyr Pro Gly Ser Pro Glu Val Leu Val
 50 55 60
 agc gga caa gat gca gct aag gcc gca att gat ata gta ggt aaa tta 240
 Ser Gly Gln Asp Ala Ala Lys Ala Ala Ile Asp Ile Val Gly Lys Leu
 65 70 75 80
 cta tca ggt tta ggg gtc cca ttt gtt ggg ccg ata gtg agt ctt tat 288
 Leu Ser Gly Leu Gly Val Pro Phe Val Gly Pro Ile Val Ser Leu Tyr
 85 90 95
 act caa ctt att gat att ctg tgg cct tca ggg gaa aag agt caa tgg 336
 Thr Gln Leu Ile Asp Ile Leu Trp Pro Ser Gly Glu Lys Ser Gln Trp
 100 105 110
 gaa att ttt atg gaa caa gta gaa gaa ctc att aat caa aaa ata gca 384
 Glu Ile Phe Met Glu Gln Val Glu Glu Leu Ile Asn Gln Lys Ile Ala
 115 120 125
 gaa tat gca agg aat aaa gcg ctt tcg gaa tta gaa gga tta ggt aat 432
 Glu Tyr Ala Arg Asn Lys Ala Leu Ser Glu Leu Glu Gly Leu Gly Asn
 130 135 140
 aat tac caa tta tat cta act gcg ctt gaa gaa tgg gaa gaa aat cca 480
 Asn Tyr Gln Leu Tyr Leu Thr Ala Leu Glu Glu Trp Glu Glu Asn Pro
 145 150 155 160
 tta aaa atg tct aga gcc tta cga gat gtg cga aat cga ttt gaa atc 528
 Leu Lys Met Ser Arg Ala Leu Arg Asp Val Arg Asn Arg Phe Glu Ile
 165 170 175
 ctg gat agt tta ttt acg caa tat atg cca tct ttt aga gtg aca aat 576
 Leu Asp Ser Leu Phe Thr Gln Tyr Met Pro Ser Phe Arg Val Thr Asn
 180 185 190
 ttt gaa gta cca ttc ctt act gta tat gca atg gca gcc aac ctt cat 624

Phe	Glu	Val	Pro	Phe	Leu	Thr	Val	Tyr	Ala	Met	Ala	Ala	Asn	Leu	His	
	195						200					205				
tta	ctg	tta	tta	aag	gac	gcg	tca	att	ttt	gga	gaa	gaa	tgg	gga	tgg	672
Leu	Leu	Leu	Leu	Lys	Asp	Ala	Ser	Ile	Phe	Gly	Glu	Glu	Trp	Gly	Trp	
	210					215				220						
tca	aca	act	act	att	aat	aac	tat	tat	gat	cgt	caa	atg	aaa	ctt	act	720
Ser	Thr	Thr	Thr	Ile	Asn	Asn	Tyr	Tyr	Asp	Arg	Gln	Met	Lys	Leu	Thr	
	225				230				235					240		
gca	gaa	tat	tct	gat	cac	tgt	gta	aag	tgg	tat	gaa	act	ggg	tta	gca	768
Ala	Glu	Tyr	Ser	Asp	His	Cys	Val	Lys	Trp	Tyr	Glu	Thr	Gly	Leu	Ala	
				245					250					255		
aaa	tta	aaa	ggc	acg	agc	gct	aaa	caa	tgg	gtt	gac	tat	aac	caa	ttc	816
Lys	Leu	Lys	Gly	Thr	Ser	Ala	Lys	Gln	Trp	Val	Asp	Tyr	Asn	Gln	Phe	
			260					265					270			
cgt	aga	gaa	atg	aca	ctg	gcg	gtt	tta	gat	gtt	gtt	gca	tta	ttc	cca	864
Arg	Arg	Glu	Met	Thr	Leu	Ala	Val	Leu	Asp	Val	Val	Ala	Leu	Phe	Pro	
		275					280					285				
aat	tat	gac	aca	cgc	acg	tac	cca	atg	gaa	acg	aaa	gca	caa	cta	aca	912
Asn	Tyr	Asp	Thr	Arg	Thr	Tyr	Pro	Met	Glu	Thr	Lys	Ala	Gln	Leu	Thr	
	290					295					300					
agg	gaa	gta	tat	aca	gat	cca	ctg	ggc	gcg	gta	aac	gtg	tct	tca	att	960
Arg	Glu	Val	Tyr	Thr	Asp	Pro	Leu	Gly	Ala	Val	Asn	Val	Ser	Ser	Ile	
	305				310					315				320		
ggg	tcc	tgg	tat	gac	aaa	gca	cct	tct	ttc	gga	gtg	ata	gaa	tca	tcc	1008
Gly	Ser	Trp	Tyr	Asp	Lys	Ala	Pro	Ser	Phe	Gly	Val	Ile	Glu	Ser	Ser	
				325					330					335		
gtt	att	cga	cca	ccc	cat	gta	ttt	gat	tat	ata	acg	gga	ctc	aca	gtg	1056
Val	Ile	Arg	Pro	Pro	His	Val	Phe	Asp	Tyr	Ile	Thr	Gly	Leu	Thr	Val	
			340					345					350			
tat	aca	caa	tca	aga	agc	att	tct	tcc	gct	cgc	tat	ata	aga	cat	tgg	1104
Tyr	Thr	Gln	Ser	Arg	Ser	Ile	Ser	Ser	Ala	Arg	Tyr	Ile	Arg	His	Trp	
		355					360					365				
gct	ggg	cat	caa	ata	agc	tac	cat	cgt	gtc	agt	agg	ggg	agt	aat	ctt	1152
Ala	Gly	His	Gln	Ile	Ser	Tyr	His	Arg	Val	Ser	Arg	Gly	Ser	Asn	Leu	
	370					375					380					
caa	caa	atg	tat	gga	act	aat	caa	aat	cta	cac	agc	act	agt	acc	ttt	1200
Gln	Gln	Met	Tyr	Gly	Thr	Asn	Gln	Asn	Leu	His	Ser	Thr	Ser	Thr	Phe	
	385				390					395					400	
gat	ttt	acg	aat	tat	gat	att	tac	aag	act	cta	tca	aag	gat	gca	gta	1248
Asp	Phe	Thr	Asn	Tyr	Asp	Ile	Tyr	Lys	Thr	Leu	Ser	Lys	Asp	Ala	Val	
			405					410						415		
ctc	ctt	gat	att	gtt	tac	cct	ggg	tat	acg	tat	ata	ttt	ttt	gga	atg	1296
Leu	Leu	Asp	Ile	Val	Tyr	Pro	Gly	Tyr	Thr	Tyr	Ile	Phe	Phe	Gly	Met	
			420					425					430			
cca	gaa	gtc	gag	ttt	ttc	atg	gta	aac	caa	ttg	aat	aat	acc	aga	aag	1344
Pro	Glu	Val	Glu	Phe	Phe	Met	Val	Asn	Gln	Leu	Asn	Asn	Thr	Arg	Lys	
		435					440					445				

acg tta aag tat aat cca gtt tcc aaa gat att ata gcg agt aca aga	1392
Thr Leu Lys Tyr Asn Pro Val Ser Lys Asp Ile Ile Ala Ser Thr Arg	
450 455 460	
gat tcg gaa tta gaa tta cct cca gaa act tca gat caa cca aat tat	1440
Asp Ser Glu Leu Glu Leu Pro Pro Glu Thr Ser Asp Gln Pro Asn Tyr	
465 470 475 480	
gag tca tat agc cat aga tta tgt cat atc aca agt att ccc gcg acg	1488
Glu Ser Tyr Ser His Arg Leu Cys His Ile Thr Ser Ile Pro Ala Thr	
485 490 495	
ggg aac act acc gga tta gta cct gta ttt tct tgg aca cat cga agt	1536
Gly Asn Thr Thr Gly Leu Val Pro Val Phe Ser Trp Thr His Arg Ser	
500 505 510	
gca gat tta aac aat aca ata tat tca gat aaa atc act caa att ccg	1584
Ala Asp Leu Asn Asn Thr Ile Tyr Ser Asp Lys Ile Thr Gln Ile Pro	
515 520 525	
gcc gtt aaa tgt tgg gat aat tta ccg ttt gtt cca gtg gta aaa gga	1632
Ala Val Lys Cys Trp Asp Asn Leu Pro Phe Val Pro Val Val Lys Gly	
530 535 540	
cca gga cat aca gga ggg gat tta tta cag tat aat aga agt act ggt	1680
Pro Gly His Thr Gly Gly Asp Leu Leu Gln Tyr Asn Arg Ser Thr Gly	
545 550 555 560	
tct gta gga acc tta ttt cta gct cga tat ggc cta gca tta gaa aaa	1728
Ser Val Gly Thr Leu Phe Leu Ala Arg Tyr Gly Leu Ala Leu Glu Lys	
565 570 575	
gca ggg aaa tat cgt gta aga ctg aga tat gct act gat gca gat att	1776
Ala Gly Lys Tyr Arg Val Arg Leu Arg Tyr Ala Thr Asp Ala Asp.Ile	
580 585 590	
gta ttg cat gta aac gat gct cag att cag atg cca aaa aca atg aac	1824
Val Leu His Val Asn Asp Ala Gln Ile Gln Met Pro Lys Thr Met Asn	
595 600 605	
cca ggt gag gat ctg aca tct aaa act ttt aaa gtt gca gat gct atc	1872
Pro Gly Glu Asp Leu Thr Ser Lys Thr Phe Lys Val Ala Asp Ala Ile	
610 615 620	
aca aca tta aat tta gca aca gat agt tcg cta gca ttg aaa cat aat	1920
Thr Thr Leu Asn Leu Ala Thr Asp Ser Ser Leu Ala Leu Lys His Asn	
625 630 635 640	
tta ggt gaa gac cct aat tca aca tta tct ggt ata gtt tac gtt gac	1968
Leu Gly Glu Asp Pro Asn Ser Thr Leu Ser Gly Ile Val Tyr Val Asp	
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Val Ser Gly Gln Asp Ala Ala Lys Ala Ala Ile Asp Ile Val Gly Lys
20 25 30

tta cta tca ggt tta ggg gtc cca ttt gtt ggg ccg ata gtg agt ctt 144
Leu Leu Ser Gly Leu Gly Val Pro Phe Val Gly Pro Ile Val Ser Leu
35 40 45

tat act caa ctt att gat att ctg tgg cct tca ggg gaa aag agt caa 192
Tyr Thr Gln Leu Ile Asp Ile Leu Trp Pro Ser Gly Glu Lys Ser Gln
50 55 60

tgg gaa att ttt atg gaa caa gta gaa gaa ctc att aat caa aaa ata 240
Trp Glu Ile Phe Met Glu Gln Val Glu Glu Ile Asn Gln Lys Ile
65 70 75 80

gca gaa tat gca agg aat aaa gcg ctt tcg gaa tta gaa gga tta ggt 288
Ala Glu Tyr Ala Arg Asn Lys Ala Leu Ser Glu Leu Glu Gly Leu Gly
85 90 95

aat aat tac caa tta tat cta act gcg ctt gaa gaa tgg gaa gaa aat 336
Asn Asn Tyr Gln Leu Tyr Leu Thr Ala Leu Glu Glu Trp Glu Glu Asn
100 105 110

cca aat ggt tca aga aat ggt tcc cgg gcc tta cga gat gtg cga aat 384
Pro Asn Gly Ser Arg Asn Gly Ser Arg Ala Leu Arg Asp Val Arg Asn
115 120 125

cga ttt gaa atc ctg gat agt tta ttt acg caa tat atg cca tct ttt 432
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Arg	Val	Thr	Asn	Phe	Glu	Val	Pro	Phe	Leu	Thr	Val	Tyr	Ala	Met	Ala		
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gcc	aac	ctt	cat	tta	ctg	tta	tta	aag	gac	gcg	tca	att	ttt	gga	gaa	528	
Ala	Asn	Leu	His	Leu	Leu	Leu	Leu	Lys	Asp	Ala	Ser	Ile	Phe	Gly	Glu		
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gaa	tgg	gga	tgg	tca	aca	act	act	att	aat	aac	tat	tat	gat	cgt	caa	576	
Glu	Trp	Gly	Trp	Ser	Thr	Thr	Thr	Ile	Asn	Asn	Tyr	Tyr	Asp	Arg	Gln		
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Met	Lys	Leu	Thr	Ala	Glu	Tyr	Ser	Asp	His	Cys	Val	Lys	Trp	Tyr	Glu		
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Thr	Gly	Leu	Ala	Lys	Leu	Lys	Gly	Thr	Ser	Ala	Lys	Gln	Trp	Val	Asp		
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Tyr	Asn	Gln	Phe	Arg	Arg	Glu	Met	Thr	Leu	Ala	Val	Leu	Asp	Val	Val		
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Ala	Leu	Phe	Pro	Asn	Tyr	Asp	Thr	Arg	Thr	Tyr	Pro	Met	Glu	Thr	Lys		
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gca	caa	cta	aca	agg	gaa	gta	tat	aca	gat	cca	ctg	ggc	gcg	gta	aac	816	
Ala	Gln	Leu	Thr	Arg	Glu	Val	Tyr	Thr	Asp	Pro	Leu	Gly	Ala	Val	Asn		
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Val	Ser	Ser	Ile	Gly	Ser	Trp	Tyr	Asp	Lys	Ala	Pro	Ser	Phe	Gly	Val		
		275					280					285					
ata	gaa	tca	tcc	gtt	att	cga	cca	ccc	cat	gta	ttt	gat	tat	ata	acg	912	
Ile	Glu	Ser	Ser	Val	Ile	Arg	Pro	Pro	His	Val	Phe	Asp	Tyr	Ile	Thr		
	290					295					300						
gga	ctc	aca	gtg	tat	aca	caa	tca	aga	agc	att	tct	tcc	gct	cgc	tat	960	
Gly	Leu	Thr	Val	Tyr	Thr	Gln	Ser	Arg	Ser	Ile	Ser	Ser	Ala	Arg	Tyr		
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ata	aga	cat	tgg	gct	ggt	cat	caa	ata	agc	tac	cat	cgt	gtc	agt	agg	1008	
Ile	Arg	His	Trp	Ala	Gly	His	Gln	Ile	Ser	Tyr	His	Arg	Val	Ser	Arg		
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ggt	agt	aat	ctt	caa	caa	atg	tat	gga	act	aat	caa	aat	cta	cac	agc	1056	
Gly	Ser	Asn	Leu	Gln	Gln	Met	Tyr	Gly	Thr	Asn	Gln	Asn	Leu	His	Ser		
			340					345					350				
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Thr	Ser	Thr	Phe	Asp	Phe	Thr	Asn	Tyr	Asp	Ile	Tyr	Lys	Thr	Leu	Ser		
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aag	gat	gca	gta	ctc	ctt	gat	att	gtt	tac	cct	ggt	tat	acg	tat	ata	1152	
Lys	Asp	Ala	Val	Leu	Leu	Asp	Ile	Val	Tyr	Pro	Gly	Tyr	Thr	Tyr	Ile		
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aat acc aga aag acg tta aag tat aat cca gtt tcc aaa gat att ata	1248
Asn Thr Arg Lys Thr Leu Lys Tyr Asn Pro Val Ser Lys Asp Ile Ile	
405 410 415	
gcg agt aca aga gat tcg gaa tta gaa tta cct cca gaa act tca gat	1296
Ala Ser Thr Arg Asp Ser Glu Leu Glu Leu Pro Pro Glu Thr Ser Asp	
420 425 430	
caa cca aat tat gag tca tat agc cat aga tta tgt cat atc aca agt	1344
Gln Pro Asn Tyr Glu Ser Tyr Ser His Arg Leu Cys His Ile Thr Ser	
435 440 445	
att ccc gcg acg ggt aac act acc gga tta gta cct gta ttt tct tgg	1392
Ile Pro Ala Thr Gly Asn Thr Thr Gly Leu Val Pro Val Phe Ser Trp	
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Thr His Arg Ser Ala Asp Leu Asn Asn Thr Ile Tyr Ser Asp Lys Ile	
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act caa att ccg gcc gtt aaa tgt tgg gat aat tta ccg ttt gtt cca	1488
Thr Gln Ile Pro Ala Val Lys Cys Trp Asp Asn Leu Pro Phe Val Pro	
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Val Val Lys Gly Pro Gly His Thr Gly Asp Leu Leu Gln Tyr Asn	
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Arg Ser Thr Gly Ser Val Gly Thr Leu Phe Leu Ala Arg Tyr Gly Leu	
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Ala Leu Glu Lys Ala Gly Lys Tyr Arg Val Arg Leu Arg Tyr Ala Thr	
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Asp Ala Asp Ile Val Leu His Val Asn Asp Ala Gln Ile Gln Met Pro	
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Lys Thr Met Asn Pro Gly Glu Asp Leu Thr Ser Lys Thr Phe Lys Val	
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Ala Asp Ala Ile Thr Thr Leu Asn Leu Ala Thr Asp Ser Ser Leu Ala	
580 585 590	
ttg aaa cat aat tta ggt gaa gac cct aat tca aca tta tct ggt ata	1824
Leu Lys His Asn Leu Gly Glu Asp Pro Asn Ser Thr Leu Ser Gly Ile	
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<212> PRT
 <213> Bacillus thuringiensis (mutated)

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 35          40          45
Tyr Thr Gln Leu Ile Asp Ile Leu Trp Pro Ser Gly Glu Lys Ser Gln
 50          55          60
Trp Glu Ile Phe Met Glu Gln Val Glu Glu Leu Ile Asn Gln Lys Ile
 65          70          75          80
Ala Glu Tyr Ala Arg Asn Lys Ala Leu Ser Glu Leu Glu Gly Leu Gly
          85          90          95
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Pro Asn Gly Ser Arg Asn Gly Ser Arg Ala Leu Arg Asp Val Arg Asn
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Arg Phe Glu Ile Leu Asp Ser Leu Phe Thr Gln Tyr Met Pro Ser Phe
 130          135          140
Arg Val Thr Asn Phe Glu Val Pro Phe Leu Thr Val Tyr Ala Met Ala
 145          150          155          160
Ala Asn Leu His Leu Leu Leu Leu Lys Asp Ala Ser Ile Phe Gly Glu
          165          170          175
Glu Trp Gly Trp Ser Thr Thr Thr Ile Asn Asn Tyr Tyr Asp Arg Gln
 180          185          190
Met Lys Leu Thr Ala Glu Tyr Ser Asp His Cys Val Lys Trp Tyr Glu
 195          200          205
Thr Gly Leu Ala Lys Leu Lys Gly Thr Ser Ala Lys Gln Trp Val Asp
 210          215          220
Tyr Asn Gln Phe Arg Arg Glu Met Thr Leu Ala Val Leu Asp Val Val
 225          230          235          240
Ala Leu Phe Pro Asn Tyr Asp Thr Arg Thr Tyr Pro Met Glu Thr Lys
          245          250          255
Ala Gln Leu Thr Arg Glu Val Tyr Thr Asp Pro Leu Gly Ala Val Asn
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Val Ser Ser Ile Gly Ser Trp Tyr Asp Lys Ala Pro Ser Phe Gly Val
 275          280          285
Ile Glu Ser Ser Val Ile Arg Pro Pro His Val Phe Asp Tyr Ile Thr
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Gly Leu Thr Val Tyr Thr Gln Ser Arg Ser Ile Ser Ser Ala Arg Tyr
 305          310          315          320
Ile Arg His Trp Ala Gly His Gln Ile Ser Tyr His Arg Val Ser Arg
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Gly Ser Asn Leu Gln Gln Met Tyr Gly Thr Asn Gln Asn Leu His Ser
          340          345          350
Thr Ser Thr Phe Asp Phe Thr Asn Tyr Asp Ile Tyr Lys Thr Leu Ser
 355          360          365
Lys Asp Ala Val Leu Leu Asp Ile Val Tyr Pro Gly Tyr Thr Tyr Ile
 370          375          380
Phe Phe Gly Met Pro Glu Val Glu Phe Phe Met Val Asn Gln Leu Asn
 385          390          395          400
Asn Thr Arg Lys Thr Leu Lys Tyr Asn Pro Val Ser Lys Asp Ile Ile
          405          410          415
Ala Ser Thr Arg Asp Ser Glu Leu Glu Leu Pro Pro Glu Thr Ser Asp
          420          425          430
Gln Pro Asn Tyr Glu Ser Tyr Ser His Arg Leu Cys His Ile Thr Ser
          435          440          445
Ile Pro Ala Thr Gly Asn Thr Thr Gly Leu Val Pro Val Phe Ser Trp
 450          455          460
Thr His Arg Ser Ala Asp Leu Asn Asn Thr Ile Tyr Ser Asp Lys Ile
  
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 Thr Gln Ile Pro Ala Val Lys Cys Trp Asp Asn Leu Pro Phe Val Pro
 485 490 495
 Val Val Lys Gly Pro Gly His Thr Gly Gly Asp Leu Leu Gln Tyr Asn
 500 505 510
 Arg Ser Thr Gly Ser Val Gly Thr Leu Phe Leu Ala Arg Tyr Gly Leu
 515 520 525
 Ala Leu Glu Lys Ala Gly Lys Tyr Arg Val Arg Leu Arg Tyr Ala Thr
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 545 550 555 560
 Lys Thr Met Asn Pro Gly Glu Asp Leu Thr Ser Lys Thr Phe Lys Val
 565 570 575
 Ala Asp Ala Ile Thr Thr Leu Asn Leu Ala Thr Asp Ser Ser Leu Ala
 580 585 590
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 595 600 605
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 610 615 620

<210> 31
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 <212> DNA
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 Val Ser Gly Gln Asp Ala Ala Lys Ala Ala Ile Asp Ile Val Gly Lys
 20 25 30

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 Leu Leu Ser Gly Leu Gly Val Pro Phe Val Gly Pro Ile Val Ser Leu
 35 40 45

 tat act caa ctt att gat att ctg tgg cct tca ggg gaa aag agt caa 192
 Tyr Thr Gln Leu Ile Asp Ile Leu Trp Pro Ser Gly Glu Lys Ser Gln
 50 55 60

 tgg gaa att ttt atg gaa caa gta gaa gaa ctc att aat caa aaa ata 240
 Trp Glu Ile Phe Met Glu Gln Val Glu Glu Leu Ile Asn Gln Lys Ile
 65 70 75 80

 gca gaa tat gca agg aat aaa gcg ctt tcg gaa tta gaa gga tta ggt 288
 Ala Glu Tyr Ala Arg Asn Lys Ala Leu Ser Glu Leu Glu Gly Leu Gly
 85 90 95

 aat aat tac caa tta tat cta act gcg ctt gaa gaa tgg gaa gaa aat 336
 Asn Asn Tyr Gln Leu Tyr Leu Thr Ala Leu Glu Glu Trp Glu Glu Asn
 100 105 110

cca tta aaa atg tct aat ggt tct aga gcc tta cga gat gtg cga aat	384
Pro Leu Lys Met Ser Asn Gly Ser Arg Ala Leu Arg Asp Val Arg Asn	
115 120 125	
cga ttt gaa atc ctg gat agt tta ttt acg caa tat atg cca tct ttt	432
Arg Phe Glu Ile Leu Asp Ser Leu Phe Thr Gln Tyr Met Pro Ser Phe	
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Arg Val Thr Asn Phe Glu Val Pro Phe Leu Thr Val Tyr Ala Met Ala	
145 150 155 160	
gcc aac ctt cat tta ctg tta tta aag gac gcg tca att ttt gga gaa	528
Ala Asn Leu His Leu Leu Leu Leu Lys Asp Ala Ser Ile Phe Gly Glu	
165 170 175	
gaa tgg gga tgg tca aca act act att aat aac tat tat gat cgt caa	576
Glu Trp Gly Trp Ser Thr Thr Thr Ile Asn Asn Tyr Tyr Asp Arg Gln	
180 185 190	
atg aaa ctt act gca gaa tat tct gat cac tgt gta aag tgg tat gaa	624
Met Lys Leu Thr Ala Glu Tyr Ser Asp His Cys Val Lys Trp Tyr Glu	
195 200 205	
act ggt tta gca aaa tta aaa ggc acg agc gct aaa caa tgg gtt gac	672
Thr Gly Leu Ala Lys Leu Lys Gly Thr Ser Ala Lys Gln Trp Val Asp	
210 215 220	
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Tyr Asn Gln Phe Arg Glu Met Thr Leu Ala Val Leu Asp Val Val	
225 230 235 240	
gca tta ttc cca aat tat gac aca cgc acg tac cca atg gaa acg aaa	768
Ala Leu Phe Pro Asn Tyr Asp Thr Arg Thr Tyr Pro Met Glu Thr Lys	
245 250 255	
gca caa cta aca agg gaa gta tat aca gat cca ctg ggc gcg gta aac	816
Ala Gln Leu Thr Arg Glu Val Tyr Thr Asp Pro Leu Gly Ala Val Asn	
260 265 270	
gtg tct tca att ggt tcc tgg tat gac aaa gca cct tct ttc gga gtg	864
Val Ser Ser Ile Gly Ser Trp Tyr Asp Lys Ala Pro Ser Phe Gly Val	
275 280 285	
ata gaa tca tcc gtt att cga cca ccc cat gta ttt gat tat ata acg	912
Ile Glu Ser Ser Val Ile Arg Pro Pro His Val Phe Asp Tyr Ile Thr	
290 295 300	
gga ctc aca gtg tat aca caa tca aga agc att tct tcc gct cgc tat	960
Gly Leu Thr Val Tyr Thr Gln Ser Arg Ser Ile Ser Ser Ala Arg Tyr	
305 310 315 320	
ata aga cat tgg gct ggt cat caa ata agc tac cat cgt gtc agt agg	1008
Ile Arg His Trp Ala Gly His Gln Ile Ser Tyr His Arg Val Ser Arg	
325 330 335	
ggt agt aat ctt caa caa atg tat gga act aat caa aat cta cac agc	1056
Gly Ser Asn Leu Gln Gln Met Tyr Gly Thr Asn Gln Asn Leu His Ser	
340 345 350	
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Thr Ser Thr Phe Asp Phe Thr Asn Tyr Asp Ile Tyr Lys Thr Leu Ser	
355 360 365	

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Lys Asp Ala Val Leu Leu Asp Ile Val Tyr Pro Gly Tyr Thr Tyr Ile	
370 375 380	
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385 390 395 400	
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405 410 415	
gcg agt aca aga gat tcg gaa tta gaa tta cct cca gaa act tca gat	1296
Ala Ser Thr Arg Asp Ser Glu Leu Glu Leu Pro Pro Glu Thr Ser Asp	
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Gln Pro Asn Tyr Glu Ser Tyr Ser His Arg Leu Cys His Ile Thr Ser	
435 440 445	
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Ile Pro Ala Thr Gly Asn Thr Thr Gly Leu Val Pro Val Phe Ser Trp	
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465 470 475 480	
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Thr Gln Ile Pro Ala Val Lys Cys Trp Asp Asn Leu Pro Phe Val Pro	
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Val Val Lys Gly Pro Gly His Thr Gly Gly Asp Leu Leu Gln Tyr Asn	
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Arg Ser Thr Gly Ser Val Gly Thr Leu Phe Leu Ala Arg Tyr Gly Leu	
515 520 525	
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Ala Leu Glu Lys Ala Gly Lys Tyr Arg Val Arg Leu Arg Tyr Ala Thr	
530 535 540	
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Asp Ala Asp Ile Val Leu His Val Asn Asp Ala Gln Ile Gln Met Pro	
545 550 555 560	
aaa aca atg aac cca ggt gag gat ctg aca tct aaa act ttt aaa gtt	1728
Lys Thr Met Asn Pro Gly Glu Asp Leu Thr Ser Lys Thr Phe Lys Val	
565 570 575	
gca gat gct atc aca aca tta aat tta gca aca gat agt tcg cta gca	1776
Ala Asp Ala Ile Thr Thr Leu Asn Leu Ala Thr Asp Ser Ser Leu Ala	
580 585 590	
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595 600 605	
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Val Tyr Val Asp Arg Ile Glu Phe Ile Pro Val Asp *	

610

615

620

<210> 32

<211> 620

<212> PRT

<213> *Bacillus thuringiensis* (mutated)

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Tyr Thr Gln Leu Ile Asp Ile Leu Trp Pro Ser Gly Glu Lys Ser Gln
          50           55           60
Trp Glu Ile Phe Met Glu Gln Val Glu Glu Leu Ile Asn Gln Lys Ile
          65           70           75           80
Ala Glu Tyr Ala Arg Asn Lys Ala Leu Ser Glu Leu Glu Gly Leu Gly
          85           90           95
Asn Asn Tyr Gln Leu Tyr Leu Thr Ala Leu Glu Glu Trp Glu Glu Asn
          100          105          110
Pro Leu Lys Met Ser Asn Gly Ser Arg Ala Leu Arg Asp Val Arg Asn
          115          120          125
Arg Phe Glu Ile Leu Asp Ser Leu Phe Thr Gln Tyr Met Pro Ser Phe
          130          135          140
Arg Val Thr Asn Phe Glu Val Pro Phe Leu Thr Val Tyr Ala Met Ala
          145          150          155          160
Ala Asn Leu His Leu Leu Leu Lys Asp Ala Ser Ile Phe Gly Glu
          165          170          175
Glu Trp Gly Trp Ser Thr Thr Thr Ile Asn Asn Tyr Tyr Asp Arg Gln
          180          185          190
Met Lys Leu Thr Ala Glu Tyr Ser Asp His Cys Val Lys Trp Tyr Glu
          195          200          205
Thr Gly Leu Ala Lys Leu Lys Gly Thr Ser Ala Lys Gln Trp Val Asp
          210          215          220
Tyr Asn Gln Phe Arg Arg Glu Met Thr Leu Ala Val Leu Asp Val Val
          225          230          235          240
Ala Leu Phe Pro Asn Tyr Asp Thr Arg Thr Tyr Pro Met Glu Thr Lys
          245          250          255
Ala Gln Leu Thr Arg Glu Val Tyr Thr Asp Pro Leu Gly Ala Val Asn
          260          265          270
Val Ser Ser Ile Gly Ser Trp Tyr Asp Lys Ala Pro Ser Phe Gly Val
          275          280          285
Ile Glu Ser Ser Val Ile Arg Pro Pro His Val Phe Asp Tyr Ile Thr
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Gly Leu Thr Val Tyr Thr Gln Ser Arg Ser Ile Ser Ser Ala Arg Tyr
          305          310          315          320
Ile Arg His Trp Ala Gly His Gln Ile Ser Tyr His Arg Val Ser Arg
          325          330          335
Gly Ser Asn Leu Gln Gln Met Tyr Gly Thr Asn Gln Asn Leu His Ser
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Thr Ser Thr Phe Asp Phe Thr Asn Tyr Asp Ile Tyr Lys Thr Leu Ser
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Lys Asp Ala Val Leu Leu Asp Ile Val Tyr Pro Gly Tyr Thr Tyr Ile
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Phe Phe Gly Met Pro Glu Val Glu Phe Phe Met Val Asn Gln Leu Asn
          385          390          395          400
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          405          410          415
Ala Ser Thr Arg Asp Ser Glu Leu Glu Leu Pro Pro Glu Thr Ser Asp
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Gln Pro Asn Tyr Glu Ser Tyr Ser His Arg Leu Cys His Ile Thr Ser
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 Ile Pro Ala Thr Gly Asn Thr Thr Gly Leu Val Pro Val Phe Ser Trp
 450 455 460
 Thr His Arg Ser Ala Asp Leu Asn Asn Thr Ile Tyr Ser Asp Lys Ile
 465 470 475 480
 Thr Gln Ile Pro Ala Val Lys Cys Trp Asp Asn Leu Pro Phe Val Pro
 485 490 495
 Val Val Lys Gly Pro Gly His Thr Gly Asp Leu Leu Gln Tyr Asn
 500 505 510
 Arg Ser Thr Gly Ser Val Gly Thr Leu Phe Leu Ala Arg Tyr Gly Leu
 515 520 525
 Ala Leu Glu Lys Ala Gly Lys Tyr Arg Val Arg Leu Arg Tyr Ala Thr
 530 535 540
 Asp Ala Asp Ile Val Leu His Val Asn Asp Ala Gln Ile Gln Met Pro
 545 550 555 560
 Lys Thr Met Asn Pro Gly Glu Asp Leu Thr Ser Lys Thr Phe Lys Val
 565 570 575
 Ala Asp Ala Ile Thr Thr Leu Asn Leu Ala Thr Asp Ser Ser Leu Ala
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 <223> LKMS.R49PVD

<400> 33
 atg tct gcg gga aat gct agt gaa tac cct ggt tca cct gaa gta ctt 48
 Met Ser Ala Gly Asn Ala Ser Glu Tyr Pro Gly Ser Pro Glu Val Leu
 1 5 10 15
 gtt agc gga caa gat gca gct aag gcc gca att gat ata gta ggt aaa 96
 Val Ser Gly Gln Asp Ala Ala Lys Ala Ala Ile Asp Ile Val Gly Lys
 20 25 30
 tta cta tca ggt tta ggg gtc cca ttt gtt ggg ccg ata gtg agt ctt 144
 Leu Leu Ser Gly Leu Gly Val Pro Phe Val Gly Pro Ile Val Ser Leu
 35 40 45
 tat act caa ctt att gat att ctg tgg cct tca ggg gaa aag agt caa 192
 Tyr Thr Gln Leu Ile Asp Ile Leu Trp Pro Ser Gly Glu Lys Ser Gln
 50 55 60
 tgg gaa att ttt atg gaa caa gta gaa gaa ctc att aat caa aaa ata 240
 Trp Glu Ile Phe Met Glu Gln Val Glu Glu Leu Ile Asn Gln Lys Ile
 65 70 75 80
 gca gaa tat gca agg aat aaa gcg ctt tcg gaa tta gaa gga tta ggt 288
 Ala Glu Tyr Ala Arg Asn Lys Ala Leu Ser Glu Leu Glu Gly Leu Gly
 85 90 95

aat aat tac caa tta tat cta act gcg ctt gaa gaa tgg gaa gaa aat	336
Asn Asn Tyr Gln Leu Tyr Leu Thr Ala Leu Glu Glu Trp Glu Glu Asn	
100 105 110	
cca tta aaa atg tct aga gcc tta cga gat gtg cga aat cga ttt gaa	384
Pro Leu Lys Met Ser Arg Ala Leu Arg Asp Val Arg Asn Arg Phe Glu	
115 120 125	
atc ctg gat agt tta ttt acg caa tat atg cca tct ttt aga gtg aca	432
Ile Leu Asp Ser Leu Phe Thr Gln Tyr Met Pro Ser Phe Arg Val Thr	
130 135 140	
aat ttt gaa gta cca ttc ctt act gta tat gca atg gca gcc aac ctt	480
Asn Phe Glu Val Pro Phe Leu Thr Val Tyr Ala Met Ala Ala Asn Leu	
145 150 155 160	
cat tta ctg tta tta aag gac gcg tca att ttt gga gaa gaa tgg gga	528
His Leu Leu Leu Leu Lys Asp Ala Ser Ile Phe Gly Glu Glu Trp Gly	
165 170 175	
tgg tca aca act act att aat aac tat tat gat cgt caa atg aaa ctt	576
Trp Ser Thr Thr Thr Ile Asn Asn Tyr Tyr Asp Arg Gln Met Lys Leu	
180 185 190	
act gca gaa tat tct gat cac tgt gta aag tgg tat gaa act ggt tta	624
Thr Ala Glu Tyr Ser Asp His Cys Val Lys Trp Tyr Glu Thr Gly Leu	
195 200 205	
gca aaa tta aaa ggc acg agc gct aaa caa tgg gtt gac tat aac caa	672
Ala Lys Leu Lys Gly Thr Ser Ala Lys Gln Trp Val Asp Tyr Asn Gln	
210 215 220	
ttc cgt aga gaa atg aca ctg gcg gtt tta gat gtt gtt gca tta ttc	720
Phe Arg Arg Glu Met Thr Leu Ala Val Leu Asp Val Val Ala Leu Phe	
225 230 235 240	
cca aat tat gac aca cgc acg tac cca atg gaa acg aaa gca caa cta	768
Pro Asn Tyr Asp Thr Arg Thr Tyr Pro Met Glu Thr Lys Ala Gln Leu	
245 250 255	
aca agg gaa gta tat aca gat cca ctg ggc gcg gta aac gtg tct tca	816
Thr Arg Glu Val Tyr Thr Asp Pro Leu Gly Ala Val Asn Val Ser Ser	
260 265 270	
att ggt tcc tgg tat gac aaa gca cct tct ttc gga gtg ata gaa tca	864
Ile Gly Ser Trp Tyr Asp Lys Ala Pro Ser Phe Gly Val Ile Glu Ser	
275 280 285	
tcc gtt att cga cca ccc cat gta ttt gat tat ata acg gga ctc aca	912
Ser Val Ile Arg Pro Pro His Val Phe Asp Tyr Ile Thr Gly Leu Thr	
290 295 300	
gtg tat aca caa tca aga agc att tct tcc gct cgc tat ata aga cat	960
Val Tyr Thr Gln Ser Arg Ser Ile Ser Ser Ala Arg Tyr Ile Arg His	
305 310 315 320	
tgg gct ggt cat caa ata agc tac cat cgt gtc agt agg ggt agt aat	1008
Trp Ala Gly His Gln Ile Ser Tyr His Arg Val Ser Arg Gly Ser Asn	
325 330 335	
ctt caa caa atg tat gga act aat caa aat cta cac agc act agt acc	1056
Leu Gln Gln Met Tyr Gly Thr Asn Gln Asn Leu His Ser Thr Ser Thr	

340	345	350	
ttt gat ttt acg aat tat gat att tac aag act cta tca aag gat gca			1104
Phe Asp Phe Thr Asn Tyr Asp Ile Tyr Lys Thr Leu Ser Lys Asp Ala			
355	360	365	
gta ctc ctt gat att gtt tac cct ggt tat acg tat ata ttt ttt gga			1152
Val Leu Leu Asp Ile Val Tyr Pro Gly Tyr Thr Tyr Ile Phe Phe Gly			
370	375	380	
atg cca gaa gtc gag ttt ttc atg gta aac caa ttg aat aat acc aga			1200
Met Pro Glu Val Glu Phe Phe Met Val Asn Gln Leu Asn Asn Thr Arg			
385	390	395	400
aag acg tta aag tat aat cca gtt tcc aaa gat att ata gcg agt aca			1248
Lys Thr Leu Lys Tyr Asn Pro Val Ser Lys Asp Ile Ile Ala Ser Thr			
405	410	415	
aga gat tcg gaa tta gaa tta cct cca gaa act tca gat caa cca aat			1296
Arg Asp Ser Glu Leu Glu Leu Pro Pro Glu Thr Ser Asp Gln Pro Asn			
420	425	430	
tat gag tca tat agc cat aga tta tgt cat atc aca agt att ccc gcg			1344
Tyr Glu Ser Tyr Ser His Arg Leu Cys His Ile Thr Ser Ile Pro Ala			
435	440	445	
acg ggt aac act acc gga tta gta cct gta ttt tct tgg aca cat cga			1392
Thr Gly Asn Thr Thr Gly Leu Val Pro Val Phe Ser Trp Thr His Arg			
450	455	460	
agt gca gat tta aac aat aca ata tat tca gat aaa atc act caa att			1440
Ser Ala Asp Leu Asn Asn Thr Ile Tyr Ser Asp Lys Ile Thr Gln Ile			
465	470	475	480
ccg gcc gtt aaa tgt tgg gat aat tta ccg ttt gtt cca gtg gta aaa			1488
Pro Ala Val Lys Cys Trp Asp Asn Leu Pro Phe Val Pro Val Val Lys			
485	490	495	
gga cca gga cat aca gga ggg gat tta tta cag tat aat aga agt act			1536
Gly Pro Gly His Thr Gly Gly Asp Leu Leu Gln Tyr Asn Arg Ser Thr			
500	505	510	
ggg tct gta gga acc tta ttt cta gct cga tat ggc cta gca tta gaa			1584
Gly Ser Val Gly Thr Leu Phe Leu Ala Arg Tyr Gly Leu Ala Leu Glu			
515	520	525	
aaa gca ggg aaa tat cgt gta aga ctg aga tat gct act gat gca gat			1632
Lys Ala Gly Lys Tyr Arg Val Arg Leu Arg Tyr Ala Thr Asp Ala Asp			
530	535	540	
att gta ttg cat gta aac gat gct cag att cag atg cca aaa aca atg			1680
Ile Val Leu His Val Asn Asp Ala Gln Ile Gln Met Pro Lys Thr Met			
545	550	555	560
aac cca ggt gag gat ctg aca tct aaa act ttt aaa gtt gca gat gct			1728
Asn Pro Gly Glu Asp Leu Thr Ser Lys Thr Phe Lys Val Ala Asp Ala			
565	570	575	
atc aca aca tta aat tta gca aca gat agt tcg cta gca ttg aaa cat			1776
Ile Thr Thr Leu Asn Leu Ala Thr Asp Ser Ser Leu Ala Leu Lys His			
580	585	590	
aat tta ggt gaa gac cct aat tca aca tta tct ggt ata gtt tac gtt			1824

Asn Leu Gly Glu Asp Pro Asn Ser Thr Leu Ser Gly Ile Val Tyr Val
 595 600 605

gac cga atc gaa ttc atc cca gta gat taa
 Asp Arg Ile Glu Phe Ile Pro Val Asp *
 610 615

1854

<210> 34
 <211> 617
 <212> PRT
 <213> Bacillus thuringiensis (mutated)

<400> 34

Met Ser Ala Gly Asn Ala Ser Glu Tyr Pro Gly Ser Pro Glu Val Leu
 1 5 10 15
 Val Ser Gly Gln Asp Ala Ala Lys Ala Ala Ile Asp Ile Val Gly Lys
 20 25 30
 Leu Leu Ser Gly Leu Gly Val Pro Phe Val Gly Pro Ile Val Ser Leu
 35 40 45
 Tyr Thr Gln Leu Ile Asp Ile Leu Trp Pro Ser Gly Glu Lys Ser Gln
 50 55 60
 Trp Glu Ile Phe Met Glu Gln Val Glu Glu Leu Ile Asn Gln Lys Ile
 65 70 75 80
 Ala Glu Tyr Ala Arg Asn Lys Ala Leu Ser Glu Leu Glu Gly Leu Gly
 85 90 95
 Asn Asn Tyr Gln Leu Tyr Leu Thr Ala Leu Glu Glu Trp Glu Glu Asn
 100 105 110
 Pro Leu Lys Met Ser Arg Ala Leu Arg Asp Val Arg Asn Arg Phe Glu
 115 120 125
 Ile Leu Asp Ser Leu Phe Thr Gln Tyr Met Pro Ser Phe Arg Val Thr
 130 135 140
 Asn Phe Glu Val Pro Phe Leu Thr Val Tyr Ala Met Ala Ala Asn Leu
 145 150 155 160
 His Leu Leu Leu Leu Lys Asp Ala Ser Ile Phe Gly Glu Glu Trp Gly
 165 170 175
 Trp Ser Thr Thr Thr Ile Asn Asn Tyr Tyr Asp Arg Gln Met Lys Leu
 180 185 190
 Thr Ala Glu Tyr Ser Asp His Cys Val Lys Trp Tyr Glu Thr Gly Leu
 195 200 205
 Ala Lys Leu Lys Gly Thr Ser Ala Lys Gln Trp Val Asp Tyr Asn Gln
 210 215 220
 Phe Arg Arg Glu Met Thr Leu Ala Val Leu Asp Val Val Ala Leu Phe
 225 230 235 240
 Pro Asn Tyr Asp Thr Arg Thr Tyr Pro Met Glu Thr Lys Ala Gln Leu
 245 250 255
 Thr Arg Glu Val Tyr Thr Asp Pro Leu Gly Ala Val Asn Val Ser Ser
 260 265 270
 Ile Gly Ser Trp Tyr Asp Lys Ala Pro Ser Phe Gly Val Ile Glu Ser
 275 280 285
 Ser Val Ile Arg Pro Pro His Val Phe Asp Tyr Ile Thr Gly Leu Thr
 290 295 300
 Val Tyr Thr Gln Ser Arg Ser Ile Ser Ser Ala Arg Tyr Ile Arg His
 305 310 315 320
 Trp Ala Gly His Gln Ile Ser Tyr His Arg Val Ser Arg Gly Ser Asn
 325 330 335
 Leu Gln Gln Met Tyr Gly Thr Asn Gln Asn Leu His Ser Thr Ser Thr
 340 345 350
 Phe Asp Phe Thr Asn Tyr Asp Ile Tyr Lys Thr Leu Ser Lys Asp Ala
 355 360 365
 Val Leu Leu Asp Ile Val Tyr Pro Gly Tyr Thr Tyr Ile Phe Phe Gly
 370 375 380
 Met Pro Glu Val Glu Phe Phe Met Val Asn Gln Leu Asn Asn Thr Arg

385 390 395 400
 Lys Thr Leu Lys Tyr Asn Pro Val Ser Lys Asp Ile Ile Ala Ser Thr
 405 410 415
 Arg Asp Ser Glu Leu Glu Leu Pro Pro Glu Thr Ser Asp Gln Pro Asn
 420 425 430
 Tyr Glu Ser Tyr Ser His Arg Leu Cys His Ile Thr Ser Ile Pro Ala
 435 440 445
 Thr Gly Asn Thr Thr Gly Leu Val Pro Val Phe Ser Trp Thr His Arg
 450 455 460
 Ser Ala Asp Leu Asn Asn Thr Ile Tyr Ser Asp Lys Ile Thr Gln Ile
 465 470 475 480
 Pro Ala Val Lys Cys Trp Asp Asn Leu Pro Phe Val Pro Val Val Lys
 485 490 495
 Gly Pro Gly His Thr Gly Gly Asp Leu Leu Gln Tyr Asn Arg Ser Thr
 500 505 510
 Gly Ser Val Gly Thr Leu Phe Leu Ala Arg Tyr Gly Leu Ala Leu Glu
 515 520 525
 Lys Ala Gly Lys Tyr Arg Val Arg Leu Arg Tyr Ala Thr Asp Ala Asp
 530 535 540
 Ile Val Leu His Val Asn Asp Ala Gln Ile Gln Met Pro Lys Thr Met
 545 550 555 560
 Asn Pro Gly Glu Asp Leu Thr Ser Lys Thr Phe Lys Val Ala Asp Ala
 565 570 575
 Ile Thr Thr Leu Asn Leu Ala Thr Asp Ser Ser Leu Ala Leu Lys His
 580 585 590
 Asn Leu Gly Glu Asp Pro Asn Ser Thr Leu Ser Gly Ile Val Tyr Val
 595 600 605
 Asp Arg Ile Glu Phe Ile Pro Val Asp
 610 615

<210> 35
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> 5' forward primer

<400> 35
 atgagtccaa ataatcaaaa tg 22

<210> 36
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> 5' reverse primer

<400> 36
 ccgcttctaa atcttggtcc 20

<210> 37
 <211> 17
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> 3' forward primer

<400> 37
 ggaacaagat ttagagg 17

<210> 38
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> 3' reverse primer

<400> 38
 ctcatcgtct acaatcaatt catc 24

<210> 39
 <211> 2022
 <212> DNA
 <213> Bacillus thuringiensis (mutated)

<220>
 <221> CDS
 <222> (1)...(2022)

<221> misc_feature
 <222> (0)...(0)
 <223> LRNS.N1218-1

<400> 39
 atg agt cca aat aat caa aat gaa tat gaa att ata gat gcg aca cct 48
 Met Ser Pro Asn Asn Gln Asn Glu Tyr Glu Ile Ile Asp Ala Thr Pro
 1 5 10 15

tct act tct gta tcc aat gat tct aac aga tac cct ttt gcg aat gag 96
 Ser Thr Ser Val Ser Asn Asp Ser Asn Arg Tyr Pro Phe Ala Asn Glu
 20 25 30

cca aca aat gcg cta caa aat atg gat tat aaa gat tat tta aaa atg 144
 Pro Thr Asn Ala Leu Gln Asn Met Asp Tyr Lys Asp Tyr Leu Lys Met
 35 40 45

tct gcg gga aat gct agt gaa tac cct ggt tca cct gaa gta ctt gtt 192
 Ser Ala Gly Asn Ala Ser Glu Tyr Pro Gly Ser Pro Glu Val Leu Val
 50 55 60

agc gga caa gat gca gct aag gcc gca att gat ata gta ggt aaa tta 240
 Ser Gly Gln Asp Ala Ala Lys Ala Ala Ile Asp Ile Val Gly Lys Leu
 65 70 75 80

cta tca ggt tta ggg gtc cca ttt gtt ggg ccg ata gtg agt ctt tat 288
 Leu Ser Gly Leu Gly Val Pro Phe Val Gly Pro Ile Val Ser Leu Tyr
 85 90 95

act caa ctt att gat att ctg tgg cct tca ggg gaa aag agt caa tgg 336
 Thr Gln Leu Ile Asp Ile Leu Trp Pro Ser Gly Glu Lys Ser Gln Trp
 100 105 110

gaa att ttt atg gaa caa gta gaa gaa ctc att aat caa aaa ata gca 384
 Glu Ile Phe Met Glu Gln Val Glu Glu Leu Ile Asn Gln Lys Ile Ala
 115 120 125

gaa tat gca agg aat aaa gcg ctt tcg gaa tta gaa gga tta ggt aat 432
 Glu Tyr Ala Arg Asn Lys Ala Leu Ser Glu Leu Glu Gly Leu Gly Asn
 130 135 140

aat tac caa tta tat cta act gcg ctt gaa gaa tgg gaa gaa aat cca 480

Asn Tyr Gln Leu Tyr Leu Thr Ala Leu Glu Glu Trp Glu Glu Asn Pro	
145 150 155 160	
tta aga atg tct aat ggt tca aga gcc tta cga gat gtg cga aat cga	528
Leu Arg Met Ser Asn Gly Ser Arg Ala Leu Arg Asp Val Arg Asn Arg	
165 170 175	
ttt gaa atc ctg gat agt tta ttt acg caa tat atg cca tct ttt aga	576
Phe Glu Ile Leu Asp Ser Leu Phe Thr Gln Tyr Met Pro Ser Phe Arg	
180 185 190	
gtg aca aat ttt gaa gta cca ttc ctt act gta tat gca atg gca gcc	624
Val Thr Asn Phe Glu Val Pro Phe Leu Thr Val Tyr Ala Met Ala Ala	
195 200 205	
aac ctt cat tta ctg tta tta aag gac gcg tca att ttt gga gaa gaa	672
Asn Leu His Leu Leu Leu Lys Asp Ala Ser Ile Phe Gly Glu Glu	
210 215 220	
tgg gga tgg tca aca act act att aat aac tat tat gat cgt caa atg	720
Trp Gly Trp Ser Thr Thr Thr Ile Asn Asn Tyr Tyr Asp Arg Gln Met	
225 230 235 240	
aaa ctt act gca gaa tat tct gat cac tgt gta aag tgg tat gaa act	768
Lys Leu Thr Ala Glu Tyr Ser Asp His Cys Val Lys Trp Tyr Glu Thr	
245 250 255	
ggg tta gca aaa tta aaa ggc acg agc gct aaa caa tgg gtt gac tat	816
Gly Leu Ala Lys Leu Lys Gly Thr Ser Ala Lys Gln Trp Val Asp Tyr	
260 265 270	
aac caa ttc cgt aga gaa atg aca ctg gcg gtt tta gat gtt gtt gca	864
Asn Gln Phe Arg Arg Glu Met Thr Leu Ala Val Leu Asp Val Val Ala	
275 280 285	
tta ttc cca aat tat gac aca cgc acg tac cca atg gaa acg aaa gca	912
Leu Phe Pro Asn Tyr Asp Thr Arg Thr Tyr Pro Met Glu Thr Lys Ala	
290 295 300	
caa cta aca agg gaa gta tat aca gat cca ctg ggc gcg gta aac gtg	960
Gln Leu Thr Arg Glu Val Tyr Thr Asp Pro Leu Gly Ala Val Asn Val	
305 310 315 320	
tct tca att ggt tcc tgg tat gac aaa gca cct tct ttc gga gtg ata	1008
Ser Ser Ile Gly Ser Trp Tyr Asp Lys Ala Pro Ser Phe Gly Val Ile	
325 330 335	
gaa tca tcc gtt att cga cca ccc cat gta ttt gat tat ata acg gga	1056
Glu Ser Ser Val Ile Arg Pro Pro His Val Phe Asp Tyr Ile Thr Gly	
340 345 350	
ctc aca gtg tat aca caa tca aga agc att tct tcc gct cgc tat ata	1104
Leu Thr Val Tyr Thr Gln Ser Arg Ser Ile Ser Ser Ala Arg Tyr Ile	
355 360 365	
aga cat tgg gct ggt cat caa ata agc tac cat cgt gtc agt agg ggt	1152
Arg His Trp Ala Gly His Gln Ile Ser Tyr His Arg Val Ser Arg Gly	
370 375 380	
agt aat ctt caa caa atg tat gga act aat caa aat cta cac agc act	1200
Ser Asn Leu Gln Gln Met Tyr Gly Thr Asn Gln Asn Leu His Ser Thr	
385 390 395 400	

agt acc ttt gat ttt acg aat tat gat att tac aag act cta tca aag	1248
Ser Thr Phe Asp Phe Thr Asn Tyr Asp Ile Tyr Lys Thr Leu Ser Lys	
405 410 415	
gat gca gta ctc ctt gat att gtt tac cct ggt tat acg tat ata ttt	1296
Asp Ala Val Leu Leu Asp Ile Val Tyr Pro Gly Tyr Thr Tyr Ile Phe	
420 425 430	
ttt gga atg cca gaa gtc gag ttt ttc atg gta aac caa ttg aat aat	1344
Phe Gly Met Pro Glu Val Glu Phe Phe Met Val Asn Gln Leu Asn Asn	
435 440 445	
acc aga aag acg tta aag tat aat cca gtt tcc aaa gat att ata gcg	1392
Thr Arg Lys Thr Leu Lys Tyr Asn Pro Val Ser Lys Asp Ile Ile Ala	
450 455 460	
agt aca aga gat tcg gaa tta gaa tta cct cca gaa act tca gat caa	1440
Ser Thr Arg Asp Ser Glu Leu Glu Leu Pro Pro Glu Thr Ser Asp Gln	
465 470 475 480	
cca aat tat gag tca tat agc cat aga tta tgt cat atc aca agt att	1488
Pro Asn Tyr Glu Ser Tyr Ser His Arg Leu Cys His Ile Thr Ser Ile	
485 490 495	
ccc gcg acg ggt aac act acc gga tta gta cct gta ttt tct tgg aca	1536
Pro Ala Thr Gly Asn Thr Thr Gly Leu Val Pro Val Phe Ser Trp Thr	
500 505 510	
cat cga agt gca gat tta aac aat aca ata tat tca gat aaa atc act	1584
His Arg Ser Ala Asp Leu Asn Asn Thr Ile Tyr Ser Asp Lys Ile Thr	
515 520 525	
caa att ccg gcc gtt aaa tgt tgg gat aat tta ccg ttt gtt cca gtg	1632
Gln Ile Pro Ala Val Lys Cys Trp Asp Asn Leu Pro Phe Val Pro Val	
530 535 540	
gta aaa gga cca gga cat aca gga ggg gat tta tta cag tat aat aga	1680
Val Lys Gly Pro Gly His Thr Gly Gly Asp Leu Leu Gln Tyr Asn Arg	
545 550 555 560	
agt act ggt tct gta gga acc tta ttt cta gct cga tat ggc cta gca	1728
Ser Thr Gly Ser Val Gly Thr Leu Phe Leu Ala Arg Tyr Gly Leu Ala	
565 570 575	
tta gaa aaa gca ggg aaa tat cgt gta aga ctg aga tat gct act gat	1776
Leu Glu Lys Ala Gly Lys Tyr Arg Val Arg Leu Arg Tyr Ala Thr Asp	
580 585 590	
gca gat att gta ttg cat gta aac gat gct cag att cag atg cca aaa	1824
Ala Asp Ile Val Leu His Val Asn Asp Ala Gln Ile Gln Met Pro Lys	
595 600 605	
aca atg aac cca ggt gag gat ctg aca tct aaa act ttt aaa gtt gca	1872
Thr Met Asn Pro Gly Glu Asp Leu Thr Ser Lys Thr Phe Lys Val Ala	
610 615 620	
gat gct atc aca aca tta aat tta gca aca gat agt tcg cta gca ttg	1920
Asp Ala Ile Thr Thr Leu Asn Leu Ala Thr Asp Ser Ser Leu Ala Leu	
625 630 635 640	
aaa cat aat tta ggt gaa gac cct aat tca aca tta tct ggt ata gtt	1968
Lys His Asn Leu Gly Glu Asp Pro Asn Ser Thr Leu Ser Gly Ile Val	
645 650 655	

tac gtt gac cga atc gaa ttc atc cca gta gat gag aca tat gaa gcg 2016
 Tyr Val Asp Arg Ile Glu Phe Ile Pro Val Asp Glu Thr Tyr Glu Ala
 660 670

gaa taa 2022
 Glu *

<210> 40
 <211> 673
 <212> PRT
 <213> Bacillus thuringiensis (mutated)

<400> 40
 Met Ser Pro Asn Asn Gln Asn Glu Tyr Glu Ile Ile Asp Ala Thr Pro
 1 5 10 15
 Ser Thr Ser Val Ser Asn Asp Ser Asn Arg Tyr Pro Phe Ala Asn Glu
 20 25 30
 Pro Thr Asn Ala Leu Gln Asn Met Asp Tyr Lys Asp Tyr Leu Lys Met
 35 40 45
 Ser Ala Gly Asn Ala Ser Glu Tyr Pro Gly Ser Pro Glu Val Leu Val
 50 55 60
 Ser Gly Gln Asp Ala Ala Lys Ala Ala Ile Asp Ile Val Gly Lys Leu
 65 70 75 80
 Leu Ser Gly Leu Gly Val Pro Phe Val Gly Pro Ile Val Ser Leu Tyr
 85 90 95
 Thr Gln Leu Ile Asp Ile Leu Trp Pro Ser Gly Glu Lys Ser Gln Trp
 100 105 110
 Glu Ile Phe Met Glu Gln Val Glu Glu Leu Ile Asn Gln Lys Ile Ala
 115 120 125
 Glu Tyr Ala Arg Asn Lys Ala Leu Ser Glu Leu Glu Gly Leu Gly Asn
 130 135 140
 Asn Tyr Gln Leu Tyr Leu Thr Ala Leu Glu Glu Trp Glu Glu Asn Pro
 145 150 155 160
 Leu Arg Met Ser Asn Gly Ser Arg Ala Leu Arg Asp Val Arg Asn Arg
 165 170 175
 Phe Glu Ile Leu Asp Ser Leu Phe Thr Gln Tyr Met Pro Ser Phe Arg
 180 185 190
 Val Thr Asn Phe Glu Val Pro Phe Leu Thr Val Tyr Ala Met Ala Ala
 195 200 205
 Asn Leu His Leu Leu Leu Leu Lys Asp Ala Ser Ile Phe Gly Glu Glu
 210 215 220
 Trp Gly Trp Ser Thr Thr Thr Ile Asn Asn Tyr Tyr Asp Arg Gln Met
 225 230 235 240
 Lys Leu Thr Ala Glu Tyr Ser Asp His Cys Val Lys Trp Tyr Glu Thr
 245 250 255
 Gly Leu Ala Lys Leu Lys Gly Thr Ser Ala Lys Gln Trp Val Asp Tyr
 260 265 270
 Asn Gln Phe Arg Arg Glu Met Thr Leu Ala Val Leu Asp Val Val Ala
 275 280 285
 Leu Phe Pro Asn Tyr Asp Thr Arg Thr Tyr Pro Met Glu Thr Lys Ala
 290 295 300
 Gln Leu Thr Arg Glu Val Tyr Thr Asp Pro Leu Gly Ala Val Asn Val
 305 310 315 320
 Ser Ser Ile Gly Ser Trp Tyr Asp Lys Ala Pro Ser Phe Gly Val Ile
 325 330 335
 Glu Ser Ser Val Ile Arg Pro Pro His Val Phe Asp Tyr Ile Thr Gly
 340 345 350
 Leu Thr Val Tyr Thr Gln Ser Arg Ser Ile Ser Ser Ala Arg Tyr Ile
 355 360 365
 Arg His Trp Ala Gly His Gln Ile Ser Tyr His Arg Val Ser Arg Gly

370	375	380
Ser Asn Leu Gln Gln Met Tyr Gly Thr Asn Gln Asn Leu His Ser Thr		
385	390	395
Ser Thr Phe Asp Phe Thr Asn Tyr Asp Ile Tyr Lys Thr Leu Ser Lys		400
	405	410
Asp Ala Val Leu Leu Asp Ile Val Tyr Pro Gly Tyr Thr Tyr Ile Phe		415
	420	425
Phe Gly Met Pro Glu Val Glu Phe Phe Met Val Asn Gln Leu Asn Asn		430
	435	440
Thr Arg Lys Thr Leu Lys Tyr Asn Pro Val Ser Lys Asp Ile Ile Ala		445
	450	455
Ser Thr Arg Asp Ser Glu Leu Glu Leu Pro Pro Glu Thr Ser Asp Gln		460
465	470	475
Pro Asn Tyr Glu Ser Tyr Ser His Arg Leu Cys His Ile Thr Ser Ile		480
	485	490
Pro Ala Thr Gly Asn Thr Thr Gly Leu Val Pro Val Phe Ser Trp Thr		495
	500	505
His Arg Ser Ala Asp Leu Asn Asn Thr Ile Tyr Ser Asp Lys Ile Thr		510
	515	520
Gln Ile Pro Ala Val Lys Cys Trp Asp Asn Leu Pro Phe Val Pro Val		525
	530	535
Val Lys Gly Pro Gly His Thr Gly Gly Asp Leu Leu Gln Tyr Asn Arg		540
545	550	555
Ser Thr Gly Ser Val Gly Thr Leu Phe Leu Ala Arg Tyr Gly Leu Ala		560
	565	570
Leu Glu Lys Ala Gly Lys Tyr Arg Val Arg Leu Arg Tyr Ala Thr Asp		575
	580	585
Ala Asp Ile Val Leu His Val Asn Asp Ala Gln Ile Gln Met Pro Lys		590
	595	600
Thr Met Asn Pro Gly Glu Asp Leu Thr Ser Lys Thr Phe Lys Val Ala		605
	610	615
Asp Ala Ile Thr Thr Leu Asn Leu Ala Thr Asp Ser Ser Leu Ala Leu		620
625	630	635
Lys His Asn Leu Gly Glu Asp Pro Asn Ser Thr Leu Ser Gly Ile Val		640
	645	650
Tyr Val Asp Arg Ile Glu Phe Ile Pro Val Asp Glu Thr Tyr Glu Ala		655
	660	665
		670
Glu		

<210> 41
 <211> 1863
 <212> DNA
 <213> Bacillus thuringiensis (mutated)

<220>
 <221> CDS
 <222> (1)...(1863)
 <221> misc_feature
 <222> (0)...(0)
 <223> LRMS.N49PVD

<400> 41	
atg tct gcg gga aat gct agt gaa tac cct ggt tca cct gaa gta ctt	48
Met Ser Ala Gly Asn Ala Ser Glu Tyr Pro Gly Ser Pro Glu Val Leu	
1 5 10 15	
ggt agc gga caa gat gca gct aag gcc gca att gat ata gta ggt aaa	96
Val Ser Gly Gln Asp Ala Ala Lys Ala Ala Ile Asp Ile Val Gly Lys	
20 25 30	

tta cta tca ggt tta ggg gtc cca ttt gtt ggg ccg ata gtg agt ctt	144
Leu Leu Ser Gly Leu Gly Val Pro Phe Val Gly Pro Ile Val Ser Leu	
35 40 45	
tat act caa ctt att gat att ctg tgg cct tca ggg gaa aag agt caa	192
Tyr Thr Gln Leu Ile Asp Ile Leu Trp Pro Ser Gly Glu Lys Ser Gln	
50 55 60	
tgg gaa att ttt atg gaa caa gta gaa gaa ctc att aat caa aaa ata	240
Trp Glu Ile Phe Met Glu Gln Val Glu Glu Ile Asn Gln Lys Ile	
65 70 75 80	
gca gaa tat gca agg aat aaa gcg ctt tcg gaa tta gaa gga tta ggt	288
Ala Glu Tyr Ala Arg Asn Lys Ala Leu Ser Glu Leu Glu Gly Leu Gly	
85 90 95	
aat aat tac caa tta tat cta act gcg ctt gaa gaa tgg gaa gaa aat	336
Asn Asn Tyr Gln Leu Tyr Leu Thr Ala Leu Glu Glu Trp Glu Glu Asn	
100 105 110	
cca tta aga atg tct aat ggt tcc cgg gcc tta cga gat gtg cga aat	384
Pro Leu Arg Met Ser Asn Gly Ser Arg Ala Leu Arg Asp Val Arg Asn	
115 120 125	
cga ttt gaa atc ctg gat agt tta ttt acg caa tat atg cca tct ttt	432
Arg Phe Glu Ile Leu Asp Ser Leu Phe Thr Gln Tyr Met Pro Ser Phe	
130 135 140	
aga gtg aca aat ttt gaa gta cca ttc ctt act gta tat gca atg gca	480
Arg Val Thr Asn Phe Glu Val Pro Phe Leu Thr Val Tyr Ala Met Ala	
145 150 155 160	
gcc aac ctt cat tta ctg tta tta aag gac gcg tca att ttt gga gaa	528
Ala Asn Leu His Leu Leu Leu Leu Lys Asp Ala Ser Ile Phe Gly Glu	
165 170 175	
gaa tgg gga tgg tca aca act act att aat aac tat tat gat cgt caa	576
Glu Trp Gly Trp Ser Thr Thr Thr Ile Asn Asn Tyr Tyr Asp Arg Gln	
180 185 190	
atg aaa ctt act gca gaa tat tct gat cac tgt gta aag tgg tat gaa	624
Met Lys Leu Thr Ala Glu Tyr Ser Asp His Cys Val Lys Trp Tyr Glu	
195 200 205	
act ggt tta gca aaa tta aaa ggc acg agc gct aaa caa tgg gtt gac	672
Thr Gly Leu Ala Lys Leu Lys Gly Thr Ser Ala Lys Gln Trp Val Asp	
210 215 220	
tat aac caa ttc cgt aga gaa atg aca ctg gcg gtt tta gat gtt gtt	720
Tyr Asn Gln Phe Arg Arg Glu Met Thr Leu Ala Val Leu Asp Val Val	
225 230 235 240	
gca tta ttc cca aat tat gac aca cgc acg tac cca atg gaa acg aaa	768
Ala Leu Phe Pro Asn Tyr Asp Thr Arg Thr Tyr Pro Met Glu Thr Lys	
245 250 255	
gca caa cta aca agg gaa gta tat aca gat cca ctg ggc gcg gta aac	816
Ala Gln Leu Thr Arg Glu Val Tyr Thr Asp Pro Leu Gly Ala Val Asn	
260 265 270	
gtg tct tca att ggt tcc tgg tat gac aaa gca cct tct ttc gga gtg	864
Val Ser Ser Ile Gly Ser Trp Tyr Asp Lys Ala Pro Ser Phe Gly Val	
275 280 285	

ata gaa tca tcc gtt att cga cca ccc cat gta ttt gat tat ata acg Ile Glu Ser Ser Val Ile Arg Pro Pro His Val Phe Asp Tyr Ile Thr 290 295 300	912
gga ctc aca gtg tat aca caa tca aga agc att tct tcc gct cgc tat Gly Leu Thr Val Tyr Thr Gln Ser Arg Ser Ile Ser Ser Ala Arg Tyr 305 310 315 320	960
ata aga cat tgg gct ggt cat caa ata agc tac cat cgt gtc agt agg Ile Arg His Trp Ala Gly His Gln Ile Ser Tyr His Arg Val Ser Arg 325 330 335	1008
ggg agt aat ctt caa caa atg tat gga act aat caa aat cta cac agc Gly Ser Asn Leu Gln Gln Met Tyr Gly Thr Asn Gln Asn Leu His Ser 340 345 350	1056
act agt acc ttt gat ttt acg aat tat gat att tac aag act cta tca Thr Ser Thr Phe Asp Phe Thr Asn Tyr Asp Ile Tyr Lys Thr Leu Ser 355 360 365	1104
aag gat gca gta ctc ctt gat att gtt tac cct ggt tat acg tat ata Lys Asp Ala Val Leu Leu Asp Ile Val Tyr Pro Gly Tyr Thr Tyr Ile 370 375 380	1152
ttt ttt gga atg cca gaa gtc gag ttt ttc atg gta aac caa ttg aat Phe Phe Gly Met Pro Glu Val Glu Phe Phe Met Val Asn Gln Leu Asn 385 390 395 400	1200
aat acc aga aag acg tta aag tat aat cca gtt tcc aaa gat att ata Asn Thr Arg Lys Thr Leu Lys Tyr Asn Pro Val Ser Lys Asp Ile Ile 405 410 415	1248
gcg agt aca aga gat tgc gaa tta gaa tta cct cca gaa act tca gat Ala Ser Thr Arg Asp Ser Glu Leu Glu Leu Pro Pro Glu Thr Ser Asp 420 425 430	1296
caa cca aat tat gag tca tat agc cat aga tta tgt cat atc aca agt Gln Pro Asn Tyr Glu Ser Tyr Ser His Arg Leu Cys His Ile Thr Ser 435 440 445	1344
att ccc gcg acg ggt aac act acc gga tta gta cct gta ttt tct tgg Ile Pro Ala Thr Gly Asn Thr Thr Gly Leu Val Pro Val Phe Ser Trp 450 455 460	1392
aca cat cga agt gca gat tta aac aat aca ata tat tca gat aaa atc Thr His Arg Ser Ala Asp Leu Asn Asn Thr Ile Tyr Ser Asp Lys Ile 465 470 475 480	1440
act caa att ccg gcc gtt aaa tgt tgg gat aat tta ccg ttt gtt cca Thr Gln Ile Pro Ala Val Lys Cys Trp Asp Asn Leu Pro Phe Val Pro 485 490 495	1488
gtg gta aaa gga cca gga cat aca gga ggg gat tta tta cag tat aat Val Val Lys Gly Pro Gly His Thr Gly Gly Asp Leu Leu Gln Tyr Asn 500 505 510	1536
aga agt act ggt tct gta gga acc tta ttt cta gct cga tat ggc cta Arg Ser Thr Gly Ser Val Gly Thr Leu Phe Leu Ala Arg Tyr Gly Leu 515 520 525	1584
gca tta gaa aaa gca ggg aaa tat cgt gta aga ctg aga tat gct act Ala Leu Glu Lys Ala Gly Lys Tyr Arg Val Arg Leu Arg Tyr Ala Thr 530 535 540 545 550	1632

530	535	540	
gat gca gat att gta ttg cat gta aac gat gct cag att cag atg cca			1680
Asp Ala Asp Ile Val Leu His Val Asn Asp Ala Gln Ile Gln Met Pro			
545	550	555	560
aaa aca atg aac cca ggt gag gat ctg aca tct aaa act ttt aaa gtt			1728
Lys Thr Met Asn Pro Gly Glu Asp Leu Thr Ser Lys Thr Phe Lys Val			
	565	570	575
gca gat gct atc aca aca tta aat tta gca aca gat agt tcg cta gca			1776
Ala Asp Ala Ile Thr Thr Leu Asn Leu Ala Thr Asp Ser Ser Leu Ala			
	580	585	590
ttg aaa cat aat tta ggt gaa gac cct aat tca aca tta tct ggt ata			1824
Leu Lys His Asn Leu Gly Glu Asp Pro Asn Ser Thr Leu Ser Gly Ile			
	595	600	605
gtt tac gtt gac cga atc gaa ttc atc cca gta gat taa			1863
Val Tyr Val Asp Arg Ile Glu Phe Ile Pro Val Asp *			
610	615	620	

<210> 42
 <211> 620
 <212> PRT
 <213> *Bacillus thuringiensis* (mutated)

<400> 42

Met Ser Ala Gly Asn Ala Ser Glu Tyr Pro Gly Ser Pro Glu Val Leu			
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Val Ser Gly Gln Asp Ala Ala Lys Ala Ala Ile Asp Ile Val Gly Lys			
	20	25	30
Leu Leu Ser Gly Leu Gly Val Pro Phe Val Gly Pro Ile Val Ser Leu			
	35	40	45
Tyr Thr Gln Leu Ile Asp Ile Leu Trp Pro Ser Gly Glu Lys Ser Gln			
	50	55	60
Trp Glu Ile Phe Met Glu Gln Val Glu Glu Leu Ile Asn Gln Lys Ile			
	65	70	75
Ala Glu Tyr Ala Arg Asn Lys Ala Leu Ser Glu Leu Glu Gly Leu Gly			
	85	90	95
Asn Asn Tyr Gln Leu Tyr Leu Thr Ala Leu Glu Glu Trp Glu Glu Asn			
	100	105	110
Pro Leu Arg Met Ser Asn Gly Ser Arg Ala Leu Arg Asp Val Arg Asn			
	115	120	125
Arg Phe Glu Ile Leu Asp Ser Leu Phe Thr Gln Tyr Met Pro Ser Phe			
	130	135	140
Arg Val Thr Asn Phe Glu Val Pro Phe Leu Thr Val Tyr Ala Met Ala			
	145	150	155
Ala Asn Leu His Leu Leu Leu Lys Asp Ala Ser Ile Phe Gly Glu			
	165	170	175
Glu Trp Gly Trp Ser Thr Thr Thr Ile Asn Asn Tyr Tyr Asp Arg Gln			
	180	185	190
Met Lys Leu Thr Ala Glu Tyr Ser Asp His Cys Val Lys Trp Tyr Glu			
	195	200	205
Thr Gly Leu Ala Lys Leu Lys Gly Thr Ser Ala Lys Gln Trp Val Asp			
	210	215	220
Tyr Asn Gln Phe Arg Arg Glu Met Thr Leu Ala Val Leu Asp Val Val			
	225	230	235
Ala Leu Phe Pro Asn Tyr Asp Thr Arg Thr Tyr Pro Met Glu Thr Lys			
	245	250	255
Ala Gln Leu Thr Arg Glu Val Tyr Thr Asp Pro Leu Gly Ala Val Asn			
	260	265	270

Val Ser Ser Ile Gly Ser Trp Tyr Asp Lys Ala Pro Ser Phe Gly Val
 275 280 285
 Ile Glu Ser Ser Val Ile Arg Pro Pro His Val Phe Asp Tyr Ile Thr
 290 295 300
 Gly Leu Thr Val Tyr Thr Gln Ser Arg Ser Ile Ser Ser Ala Arg Tyr
 305 310 315 320
 Ile Arg His Trp Ala Gly His Gln Ile Ser Tyr His Arg Val Ser Arg
 325 330 335
 Gly Ser Asn Leu Gln Gln Met Tyr Gly Thr Asn Gln Asn Leu His Ser
 340 345 350
 Thr Ser Thr Phe Asp Phe Thr Asn Tyr Asp Ile Tyr Lys Thr Leu Ser
 355 360 365
 Lys Asp Ala Val Leu Leu Asp Ile Val Tyr Pro Gly Tyr Thr Tyr Ile
 370 375 380
 Phe Phe Gly Met Pro Glu Val Glu Phe Phe Met Val Asn Gln Leu Asn
 385 390 395 400
 Asn Thr Arg Lys Thr Leu Lys Tyr Asn Pro Val Ser Lys Asp Ile Ile
 405 410 415
 Ala Ser Thr Arg Asp Ser Glu Leu Glu Leu Pro Pro Glu Thr Ser Asp
 420 425 430
 Gln Pro Asn Tyr Glu Ser Tyr Ser His Arg Leu Cys His Ile Thr Ser
 435 440 445
 Ile Pro Ala Thr Gly Asn Thr Thr Gly Leu Val Pro Val Phe Ser Trp
 450 455 460
 Thr His Arg Ser Ala Asp Leu Asn Asn Thr Ile Tyr Ser Asp Lys Ile
 465 470 475 480
 Thr Gln Ile Pro Ala Val Lys Cys Trp Asp Asn Leu Pro Phe Val Pro
 485 490 495
 Val Val Lys Gly Pro Gly His Thr Gly Gly Asp Leu Leu Gln Tyr Asn
 500 505 510
 Arg Ser Thr Gly Ser Val Gly Thr Leu Phe Leu Ala Arg Tyr Gly Leu
 515 520 525
 Ala Leu Glu Lys Ala Gly Lys Tyr Arg Val Arg Leu Arg Tyr Ala Thr
 530 535 540
 Asp Ala Asp Ile Val Leu His Val Asn Asp Ala Gln Ile Gln Met Pro
 545 550 555 560
 Lys Thr Met Asn Pro Gly Glu Asp Leu Thr Ser Lys Thr Phe Lys Val
 565 570 575
 Ala Asp Ala Ile Thr Thr Leu Asn Leu Ala Thr Asp Ser Ser Leu Ala
 580 585 590
 Leu Lys His Asn Leu Gly Glu Asp Pro Asn Ser Thr Leu Ser Gly Ile
 595 600 605
 Val Tyr Val Asp Arg Ile Glu Phe Ile Pro Val Asp
 610 615 620

<210> 43
 <211> 2013
 <212> DNA
 <213> Bacillus thuringiensis (mutated)

<220>
 <221> CDS
 <222> (1)...(2013)

<221> misc_feature
 <222> (0)...(0)
 <223> LRMS.R1218-1

<400> 43
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 Met Ser Pro Asn Asn Gln Asn Glu Tyr Glu Ile Ile Asp Ala Thr Pro
 1 5 10 15

tct act tct gta tcc aat gat tct aac aga tac cct ttt gcg aat gag	96
Ser Thr Ser Val Ser Asn Asp Ser Asn Arg Tyr Pro Phe Ala Asn Glu	
20 25 30	
cca aca aat gcg cta caa aat atg gat tat aaa gat tat tta aaa atg	144
Pro Thr Asn Ala Leu Gln Asn Met Asp Tyr Lys Asp Tyr Leu Lys Met	
35 40 45	
tct gcg gga aat gct agt gaa tac cct ggt tca cct gaa gta ctt gtt	192
Ser Ala Gly Asn Ala Ser Glu Tyr Pro Gly Ser Pro Glu Val Leu Val	
50 55 60	
agc gga caa gat gca gct aag gcc gca att gat ata gta ggt aaa tta	240
Ser Gly Gln Asp Ala Ala Lys Ala Ala Ile Asp Ile Val Gly Lys Leu	
65 70 75 80	
cta tca ggt tta ggg gtc cca ttt gtt ggg ccg ata gtg agt ctt tat	288
Leu Ser Gly Leu Gly Val Pro Phe Val Gly Pro Ile Val Ser Leu Tyr	
85 90 95	
act caa ctt att gat att ctg tgg cct tca ggg gaa aag agt caa tgg	336
Thr Gln Leu Ile Asp Ile Leu Trp Pro Ser Gly Glu Lys Ser Gln Trp	
100 105 110	
gaa att ttt atg gaa caa gta gaa gaa ctc att aat caa aaa ata gca	384
Glu Ile Phe Met Glu Gln Val Glu Glu Leu Ile Asn Gln Lys Ile Ala	
115 120 125	
gaa tat gca agg aat aaa gcg ctt tcg gaa tta gaa gga tta ggt aat	432
Glu Tyr Ala Arg Asn Lys Ala Leu Ser Glu Leu Glu Gly Leu Gly Asn	
130 135 140	
aat tac caa tta tat cta act gcg ctt gaa gaa tgg gaa gaa aat cca	480
Asn Tyr Gln Leu Tyr Leu Thr Ala Leu Glu Glu Trp Glu Glu Asn Pro	
145 150 155 160	
tta aga atg tct aga gcc tta cga gat gtg cga aat cga ttt gaa atc	528
Leu Arg Met Ser Arg Ala Leu Arg Asp Val Arg Asn Arg Phe Glu Ile	
165 170 175	
ctg gat agt tta ttt acg caa tat atg cca tct ttt aga gtg aca aat	576
Leu Asp Ser Leu Phe Thr Gln Tyr Met Pro Ser Phe Arg Val Thr Asn	
180 185 190	
ttt gaa gta cca ttc ctt act gta tat gca atg gca gcc aac ctt cat	624
Phe Glu Val Pro Phe Leu Thr Val Tyr Ala Met Ala Ala Asn Leu His	
195 200 205	
tta ctg tta tta aag gac gcg tca att ttt gga gaa gaa tgg gga tgg	672
Leu Leu Leu Leu Lys Asp Ala Ser Ile Phe Gly Glu Glu Trp Gly Trp	
210 215 220	
tca aca act act att aat aac tat tat gat cgt caa atg aaa ctt act	720
Ser Thr Thr Thr Ile Asn Asn Tyr Tyr Asp Arg Gln Met Lys Leu Thr	
225 230 235 240	
gca gaa tat tct gat cac tgt gta aag tgg tat gaa act ggt tta gca	768
Ala Glu Tyr Ser Asp His Cys Val Lys Trp Tyr Glu Thr Gly Leu Ala	
245 250 255	
aaa tta aaa ggc acg agc gct aaa caa tgg gtt gac tat aac caa ttc	816
Lys Leu Lys Gly Thr Ser Ala Lys Gln Trp Val Asp Tyr Asn Gln Phe	

260	265	270	
cgt aga gaa atg aca ctg gcg gtt tta gat gtt gtt gca tta ttc cca			864
Arg Arg Glu Met Thr Leu Ala Val Leu Asp Val Val Ala Leu Phe Pro			
275	280	285	
aat tat gac aca cgc acg tac cca atg gaa acg aaa gca caa cta aca			912
Asn Tyr Asp Thr Arg Thr Tyr Pro Met Glu Thr Lys Ala Gln Leu Thr			
290	295	300	
agg gaa gta tat aca gat cca ctg ggc gcg gta aac gtg tct tca att			960
Arg Glu Val Tyr Thr Asp Pro Leu Gly Ala Val Asn Val Ser Ser Ile			
305	310	315	320
ggt tcc tgg tat gac aaa gca cct tct ttc gga gtg ata gaa tca tcc			1008
Gly Ser Trp Tyr Asp Lys Ala Pro Ser Phe Gly Val Ile Glu Ser Ser			
325	330	335	
gtt att cga cca ccc cat gta ttt gat tat ata acg gga ctc aca gtg			1056
Val Ile Arg Pro Pro His Val Phe Asp Tyr Ile Thr Gly Leu Thr Val			
340	345	350	
tat aca caa tca aga agc att tct tcc gct cgc tat ata aga cat tgg			1104
Tyr Thr Gln Ser Arg Ser Ile Ser Ser Ala Arg Tyr Ile Arg His Trp			
355	360	365	
gct ggt cat caa ata agc tac cat cgt gtc agt agg ggt agt aat ctt			1152
Ala Gly His Gln Ile Ser Tyr His Arg Val Ser Arg Gly Ser Asn Leu			
370	375	380	
caa caa atg tat gga act aat caa aat cta cac agc act agt acc ttt			1200
Gln Gln Met Tyr Gly Thr Asn Gln Asn Leu His Ser Thr Ser Thr Phe			
385	390	395	400
gat ttt acg aat tat gat att tac aag act cta tca aag gat gca gta			1248
Asp Phe Thr Asn Tyr Asp Ile Tyr Lys Thr Leu Ser Lys Asp Ala Val			
405	410	415	
ctc ctt gat att gtt tac cct ggt tat acg tat ata ttt ttt gga atg			1296
Leu Leu Asp Ile Val Tyr Pro Gly Tyr Thr Tyr Ile Phe Phe Gly Met			
420	425	430	
cca gaa gtc gag ttt ttc atg gta aac caa ttg aat aat acc aga aag			1344
Pro Glu Val Glu Phe Phe Met Val Asn Gln Leu Asn Asn Thr Arg Lys			
435	440	445	
acg tta aag tat aat cca gtt tcc aaa gat att ata gcg agt aca aga			1392
Thr Leu Lys Tyr Asn Pro Val Ser Lys Asp Ile Ile Ala Ser Thr Arg			
450	455	460	
gat tcg gaa tta gaa tta cct cca gaa act tca gat caa cca aat tat			1440
Asp Ser Glu Leu Glu Leu Pro Pro Glu Thr Ser Asp Gln Pro Asn Tyr			
465	470	475	480
gag tca tat agc cat aga tta tgt cat atc aca agt att ccc gcg acg			1488
Glu Ser Tyr Ser His Arg Leu Cys His Ile Thr Ser Ile Pro Ala Thr			
485	490	495	
ggt aac act acc gga tta gta cct gta ttt tct tgg aca cat cga agt			1536
Gly Asn Thr Thr Gly Leu Val Pro Val Phe Ser Trp Thr His Arg Ser			
500	505	510	
gca gat tta aac aat aca ata tat tca gat aaa atc act caa att ccg			1584

Ala Asp Leu Asn Asn Thr Ile Tyr Ser Asp Lys Ile Thr Gln Ile Pro	
515 520 525	
gcc gtt aaa tgt tgg gat aat tta ccg ttt gtt cca gtg gta aaa gga	1632
Ala Val Lys Cys Trp Asp Asn Leu Pro Phe Val Pro Val Val Lys Gly	
530 535 540	
cca gga cat aca gga ggg gat tta tta cag tat aat aga agt act ggt	1680
Pro Gly His Thr Gly Gly Asp Leu Leu Gln Tyr Asn Arg Ser Thr Gly	
545 550 555 560	
tct gta gga acc tta ttt cta gct cga tat ggc cta gca tta gaa aaa	1728
Ser Val Gly Thr Leu Phe Leu Ala Arg Tyr Gly Leu Ala Leu Glu Lys	
565 570 575	
gca ggg aaa tat cgt gta aga ctg aga tat gct act gat gca gat att	1776
Ala Gly Lys Tyr Arg Val Arg Leu Arg Tyr Ala Thr Asp Ala Asp Ile	
580 585 590	
gta ttg cat gta aac gat gct cag att cag atg cca aaa aca atg aac	1824
Val Leu His Val Asn Asp Ala Gln Ile Gln Met Pro Lys Thr Met Asn	
595 600 605	
cca ggt gag gat ctg aca tct aaa act ttt aaa gtt gca gat gct atc	1872
Pro Gly Glu Asp Leu Thr Ser Lys Thr Phe Lys Val Ala Asp Ala Ile	
610 615 620	
aca aca tta aat tta gca aca gat agt tcg cta gca ttg aaa cat aat	1920
Thr Thr Leu Asn Leu Ala Thr Asp Ser Ser Leu Ala Leu Lys His Asn	
625 630 635 640	
tta ggt gaa gac cct aat tca aca tta tct ggt ata gtt tac gtt gac	1968
Leu Gly Glu Asp Pro Asn Ser Thr Leu Ser Gly Ile Val Tyr Val Asp	
645 650 655	
cga atc gaa ttc atc cca gta gat gag aca tat gaa gcg gaa taa	2013
Arg Ile Glu Phe Ile Pro Val Asp Glu Thr Tyr Glu Ala Glu *	
660 665 670	

<210> 44
 <211> 670
 <212> PRT
 <213> Bacillus thuringiensis (mutated)

<400> 44

Met Ser Pro Asn Asn Gln Asn Glu Tyr Glu Ile Ile Asp Ala Thr Pro	
1 5 10 15	
Ser Thr Ser Val Ser Asn Asp Ser Asn Arg Tyr Pro Phe Ala Asn Glu	
20 25 30	
Pro Thr Asn Ala Leu Gln Asn Met Asp Tyr Lys Asp Tyr Leu Lys Met	
35 40 45	
Ser Ala Gly Asn Ala Ser Glu Tyr Pro Gly Ser Pro Glu Val Leu Val	
50 55 60	
Ser Gly Gln Asp Ala Ala Lys Ala Ala Ile Asp Ile Val Gly Lys Leu	
65 70 75 80	
Leu Ser Gly Leu Gly Val Pro Phe Val Gly Pro Ile Val Ser Leu Tyr	
85 90 95	
Thr Gln Leu Ile Asp Ile Leu Trp Pro Ser Gly Glu Lys Ser Gln Trp	
100 105 110	
Glu Ile Phe Met Glu Gln Val Glu Glu Leu Ile Asn Gln Lys Ile Ala	
115 120 125	

Glu	Tyr	Ala	Arg	Asn	Lys	Ala	Leu	Ser	Glu	Leu	Glu	Gly	Leu	Gly	Asn	
130						135					140					
Asn	Tyr	Gln	Leu	Tyr	Leu	Thr	Ala	Leu	Glu	Glu	Trp	Glu	Glu	Asn	Pro	
145					150					155					160	
Leu	Arg	Met	Ser	Arg	Ala	Leu	Arg	Asp	Val	Arg	Asn	Arg	Phe	Glu	Ile	
				165					170					175		
Leu	Asp	Ser	Leu	Phe	Thr	Gln	Tyr	Met	Pro	Ser	Phe	Arg	Val	Thr	Asn	
			180					185					190			
Phe	Glu	Val	Pro	Phe	Leu	Thr	Val	Tyr	Ala	Met	Ala	Ala	Asn	Leu	His	
	195						200					205				
Leu	Leu	Leu	Leu	Lys	Asp	Ala	Ser	Ile	Phe	Gly	Glu	Glu	Trp	Gly	Trp	
	210					215				220						
Ser	Thr	Thr	Thr	Ile	Asn	Asn	Tyr	Tyr	Asp	Arg	Gln	Met	Lys	Leu	Thr	
225					230					235					240	
Ala	Glu	Tyr	Ser	Asp	His	Cys	Val	Lys	Trp	Tyr	Glu	Thr	Gly	Leu	Ala	
				245					250					255		
Lys	Leu	Lys	Gly	Thr	Ser	Ala	Lys	Gln	Trp	Val	Asp	Tyr	Asn	Gln	Phe	
		260						265					270			
Arg	Arg	Glu	Met	Thr	Leu	Ala	Val	Leu	Asp	Val	Val	Ala	Leu	Phe	Pro	
		275					280					285				
Asn	Tyr	Asp	Thr	Arg	Thr	Tyr	Pro	Met	Glu	Thr	Lys	Ala	Gln	Leu	Thr	
	290					295					300					
Arg	Glu	Val	Tyr	Thr	Asp	Pro	Leu	Gly	Ala	Val	Asn	Val	Ser	Ser	Ile	
305					310					315					320	
Gly	Ser	Trp	Tyr	Asp	Lys	Ala	Pro	Ser	Phe	Gly	Val	Ile	Glu	Ser	Ser	
				325					330					335		
Val	Ile	Arg	Pro	Pro	His	Val	Phe	Asp	Tyr	Ile	Thr	Gly	Leu	Thr	Val	
		340						345					350			
Tyr	Thr	Gln	Ser	Arg	Ser	Ile	Ser	Ser	Ala	Arg	Tyr	Ile	Arg	His	Trp	
	355						360					365				
Ala	Gly	His	Gln	Ile	Ser	Tyr	His	Arg	Val	Ser	Arg	Gly	Ser	Asn	Leu	
	370					375					380					
Gln	Gln	Met	Tyr	Gly	Thr	Asn	Gln	Asn	Leu	His	Ser	Thr	Ser	Thr	Phe	
385					390					395					400	
Asp	Phe	Thr	Asn	Tyr	Asp	Ile	Tyr	Lys	Thr	Leu	Ser	Lys	Asp	Ala	Val	
				405					410					415		
Leu	Leu	Asp	Ile	Val	Tyr	Pro	Gly	Tyr	Thr	Tyr	Ile	Phe	Phe	Gly	Met	
		420					425						430			
Pro	Glu	Val	Glu	Phe	Phe	Met	Val	Asn	Gln	Leu	Asn	Asn	Thr	Arg	Lys	
		435					440					445				
Thr	Leu	Lys	Tyr	Asn	Pro	Val	Ser	Lys	Asp	Ile	Ile	Ala	Ser	Thr	Arg	
	450					455					460					
Asp	Ser	Glu	Leu	Glu	Leu	Pro	Pro	Glu	Thr	Ser	Asp	Gln	Pro	Asn	Tyr	
465					470					475					480	
Glu	Ser	Tyr	Ser	His	Arg	Leu	Cys	His	Ile	Thr	Ser	Ile	Pro	Ala	Thr	
				485					490					495		
Gly	Asn	Thr	Thr	Gly	Leu	Val	Pro	Val	Phe	Ser	Trp	Thr	His	Arg	Ser	
		500						505					510			
Ala	Asp	Leu	Asn	Asn	Thr	Ile	Tyr	Ser	Asp	Lys	Ile	Thr	Gln	Ile	Pro	
	515						520					525				
Ala	Val	Lys	Cys	Trp	Asp	Asn	Leu	Pro	Phe	Val	Pro	Val	Val	Lys	Gly	
	530					535					540					
Pro	Gly	His	Thr	Gly	Gly	Asp	Leu	Leu	Gln	Tyr	Asn	Arg	Ser	Thr	Gly	
545					550					555					560	
Ser	Val	Gly	Thr	Leu	Phe	Leu	Ala	Arg	Tyr	Gly	Leu	Ala	Leu	Glu	Lys	
				565					570					575		
Ala	Gly	Lys	Tyr	Arg	Val	Arg	Leu	Arg	Tyr	Ala	Thr	Asp	Ala	Asp	Ile	
		580					585					590				
Val	Leu	His	Val	Asn	Asp	Ala	Gln	Ile	Gln	Met	Pro	Lys	Thr	Met	Asn	
		595					600					605				
Pro	Gly	Glu	Asp	Leu	Thr	Ser	Lys	Thr	Phe	Lys	Val	Ala	Asp	Ala	Ile	
	610						615				620					
Thr	Thr	Leu	Asn	Leu	Ala	Thr	Asp	Ser	Ser	Leu	Ala	Leu	Lys	His	Asn	

625 630 635 640
 Leu Gly Glu Asp Pro Asn Ser Thr Leu Ser Gly Ile Val Tyr Val Asp
 645 650 655
 Arg Ile Glu Phe Ile Pro Val Asp Glu Thr Tyr Glu Ala Glu
 660 665 670

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 <211> 1854
 <212> DNA
 <213> *Bacillus thuringiensis* (mutated)

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 Met Ser Ala Gly Asn Ala Ser Glu Tyr Pro Gly Ser Pro Glu Val Leu
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 gtt agc gga caa gat gca gct aag gcc gca att gat ata gta ggt aaa 96
 Val Ser Gly Gln Asp Ala Ala Lys Ala Ala Ile Asp Ile Val Gly Lys
 20 25 30

 tta cta tca ggt tta ggg gtc cca ttt gtt ggg ccg ata gtg agt ctt 144
 Leu Leu Ser Gly Leu Gly Val Pro Phe Val Gly Pro Ile Val Ser Leu
 35 40 45

 tat act caa ctt att gat att ctg tgg cct tca ggg gaa aag agt caa 192
 Tyr Thr Gln Leu Ile Asp Ile Leu Trp Pro Ser Gly Glu Lys Ser Gln
 50 55 60

 tgg gaa att ttt atg gaa caa gta gaa gaa ctc att aat caa aaa ata 240
 Trp Glu Ile Phe Met Glu Gln Val Glu Glu Leu Ile Asn Gln Lys Ile
 65 70 75 80

 gca gaa tat gca agg aat aaa gcg ctt tcg gaa tta gaa gga tta ggt 288
 Ala Glu Tyr Ala Arg Asn Lys Ala Leu Ser Glu Leu Glu Gly Leu Gly
 85 90 95

 aat aat tac caa tta tat cta act gcg ctt gaa gaa tgg gaa gaa aat 336
 Asn Asn Tyr Gln Leu Tyr Leu Thr Ala Leu Glu Glu Trp Glu Glu Asn
 100 105 110

 cca tta aga atg tct aga gcc tta cga gat gtg cga aat cga ttt gaa 384
 Pro Leu Arg Met Ser Arg Ala Leu Arg Asp Val Arg Asn Arg Phe Glu
 115 120 125

 atc ctg gat agt tta ttt acg caa tat atg cca tct ttt aga gtg aca 432
 Ile Leu Asp Ser Leu Phe Thr Gln Tyr Met Pro Ser Phe Arg Val Thr
 130 135 140

 aat ttt gaa gta cca ttc ctt act gta tat gca atg gca gcc aac ctt 480
 Asn Phe Glu Val Pro Phe Leu Thr Val Tyr Ala Met Ala Ala Asn Leu
 145 150 155 160

 cat tta ctg tta tta aag gac gcg tca att ttt gga gaa gaa tgg gga 528
 His Leu Leu Leu Leu Lys Asp Ala Ser Ile Phe Gly Glu Glu Trp Gly

165	170	175	
tgg tca aca act act att aat aac tat tat gat cgt caa atg aaa ctt			576
Trp Ser Thr Thr Thr Ile Asn Asn Tyr Tyr Asp Arg Gln Met Lys Leu			
180	185	190	
act gca gaa tat tct gat cac tgt gta aag tgg tat gaa act ggt tta			624
Thr Ala Glu Tyr Ser Asp His Cys Val Lys Trp Tyr Glu Thr Gly Leu			
195	200	205	
gca aaa tta aaa ggc acg agc gct aaa caa tgg gtt gac tat aac caa			672
Ala Lys Leu Lys Gly Thr Ser Ala Lys Gln Trp Val Asp Tyr Asn Gln			
210	215	220	
ttc cgt aga gaa atg aca ctg gcg gtt tta gat gtt gtt gca tta ttc			720
Phe Arg Arg Glu Met Thr Leu Ala Val Leu Asp Val Val Ala Leu Phe			
225	230	235	240
cca aat tat gac aca cgc acg tac cca atg gaa acg aaa gca caa cta			768
Pro Asn Tyr Asp Thr Arg Thr Tyr Pro Met Glu Thr Lys Ala Gln Leu			
245	250	255	
aca agg gaa gta tat aca gat cca ctg ggc gcg gta aac gtg tct tca			816
Thr Arg Glu Val Tyr Thr Asp Pro Leu Gly Ala Val Asn Val Ser Ser			
260	265	270	
att ggt tcc tgg tat gac aaa gca cct tct ttc gga gtg ata gaa tca			864
Ile Gly Ser Trp Tyr Asp Lys Ala Pro Ser Phe Gly Val Ile Glu Ser			
275	280	285	
tcc gtt att cga cca ccc cat gta ttt gat tat ata acg gga ctc aca			912
Ser Val Ile Arg Pro Pro His Val Phe Asp Tyr Ile Thr Gly Leu Thr			
290	295	300	
gtg tat aca caa tca aga agc att tct tcc gct cgc tat ata aga cat			960
Val Tyr Thr Gln Ser Arg Ser Ile Ser Ser Ala Arg Tyr Ile Arg His			
305	310	315	320
tgg gct ggt cat caa ata agc tac cat cgt gtc agt agg ggt agt aat			1008
Trp Ala Gly His Gln Ile Ser Tyr His Arg Val Ser Arg Gly Ser Asn			
325	330	335	
ctt caa caa atg tat gga act aat caa aat cta cac agc act agt acc			1056
Leu Gln Gln Met Tyr Gly Thr Asn Gln Asn Leu His Ser Thr Ser Thr			
340	345	350	
ttt gat ttt acg aat tat gat att tac aag act cta tca aag gat gca			1104
Phe Asp Phe Thr Asn Tyr Asp Ile Tyr Lys Thr Leu Ser Lys Asp Ala			
355	360	365	
gta ctc ctt gat att gtt tac cct ggt tat acg tat ata ttt ttt gga			1152
Val Leu Leu Asp Ile Val Tyr Pro Gly Tyr Thr Tyr Ile Phe Phe Gly			
370	375	380	
atg cca gaa gtc gag ttt ttc atg gta aac caa ttg aat aat acc aga			1200
Met Pro Glu Val Glu Phe Phe Met Val Asn Gln Leu Asn Asn Thr Arg			
385	390	395	400
aag acg tta aag tat aat cca gtt tcc aaa gat att ata gcg agt aca			1248
Lys Thr Leu Lys Tyr Asn Pro Val Ser Lys Asp Ile Ile Ala Ser Thr			
405	410	415	
aga gat tcg gaa tta gaa tta cct cca gaa act tca gat caa cca aat			1296

Arg Asp Ser Glu Leu Glu Leu Pro Pro Glu Thr Ser Asp Gln Pro Asn	
420 425 430	
tat gag tca tat agc cat aga tta tgt cat atc aca agt att ccc gcg	1344
Tyr Glu Ser Tyr Ser His Arg Leu Cys His Ile Thr Ser Ile Pro Ala	
435 440 445	
acg ggt aac act acc gga tta gta cct gta ttt tct tgg aca cat cga	1392
Thr Gly Asn Thr Thr Gly Leu Val Pro Val Phe Ser Trp Thr His Arg	
450 455 460	
agt gca gat tta aac aat aca ata tat tca gat aaa atc act caa att	1440
Ser Ala Asp Leu Asn Asn Thr Ile Tyr Ser Asp Lys Ile Thr Gln Ile	
465 470 475 480	
ccg gcc gtt aaa tgt tgg gat aat tta ccg ttt gtt cca gtg gta aaa	1488
Pro Ala Val Lys Cys Trp Asp Asn Leu Pro Phe Val Pro Val Val Lys	
485 490 495	
gga cca gga cat aca gga ggg gat tta tta cag tat aat aga agt act	1536
Gly Pro Gly His Thr Gly Gly Asp Leu Leu Gln Tyr Asn Arg Ser Thr	
500 505 510	
ggg tct gta gga acc tta ttt cta gct cga tat ggc cta gca tta gaa	1584
Gly Ser Val Gly Thr Leu Phe Leu Ala Arg Tyr Gly Leu Ala Leu Glu	
515 520 525	
aaa gca ggg aaa tat cgt gta aga ctg aga tat gct act gat gca gat	1632
Lys Ala Gly Lys Tyr Arg Val Arg Leu Arg Tyr Ala Thr Asp Ala Asp	
530 535 540	
att gta ttg cat gta aac gat gct cag att cag atg cca aaa aca atg	1680
Ile Val Leu His Val Asn Asp Ala Gln Ile Gln Met Pro Lys Thr Met	
545 550 555 560	
aac cca ggt gag gat ctg aca tct aaa act ttt aaa gtt gca gat gct	1728
Asn Pro Gly Glu Asp Leu Thr Ser Lys Thr Phe Lys Val Ala Asp Ala	
565 570 575	
atc aca aca tta aat tta gca aca gat agt tcg cta gca ttg aaa cat	1776
Ile Thr Thr Leu Asn Leu Ala Thr Asp Ser Ser Leu Ala Leu Lys His	
580 585 590	
aat tta ggt gaa gac cct aat tca aca tta tct ggt ata gtt tac gtt	1824
Asn Leu Gly Glu Asp Pro Asn Ser Thr Leu Ser Gly Ile Val Tyr Val	
595 600 605	
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Asp Arg Ile Glu Phe Ile Pro Val Asp *	
610 615	

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 <212> PRT
 <213> Bacillus thuringiensis (mutated)

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 20 25 30
 Leu Leu Ser Gly Leu Gly Val Pro Phe Val Gly Pro Ile Val Ser Leu

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Tyr	Thr	Gln	Leu	Ile	Asp	Ile	Leu	Trp	Pro	Ser	Gly	Glu	Lys	Ser	Gln	
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Trp	Glu	Ile	Phe	Met	Glu	Gln	Val	Glu	Glu	Leu	Ile	Asn	Gln	Lys	Ile	
65				70					75						80	
Ala	Glu	Tyr	Ala	Arg	Asn	Lys	Ala	Leu	Ser	Glu	Leu	Glu	Gly	Leu	Gly	
				85					90					95		
Asn	Asn	Tyr	Gln	Leu	Tyr	Leu	Thr	Ala	Leu	Glu	Glu	Trp	Glu	Glu	Asn	
			100					105					110			
Pro	Leu	Arg	Met	Ser	Arg	Ala	Leu	Arg	Asp	Val	Arg	Asn	Arg	Phe	Glu	
		115				120					125					
Ile	Leu	Asp	Ser	Leu	Phe	Thr	Gln	Tyr	Met	Pro	Ser	Phe	Arg	Val	Thr	
	130					135					140					
Asn	Phe	Glu	Val	Pro	Phe	Leu	Thr	Val	Tyr	Ala	Met	Ala	Ala	Asn	Leu	
145					150					155					160	
His	Leu	Leu	Leu	Leu	Lys	Asp	Ala	Ser	Ile	Phe	Gly	Glu	Glu	Trp	Gly	
				165					170					175		
Trp	Ser	Thr	Thr	Thr	Ile	Asn	Asn	Tyr	Tyr	Asp	Arg	Gln	Met	Lys	Leu	
			180					185					190			
Thr	Ala	Glu	Tyr	Ser	Asp	His	Cys	Val	Lys	Trp	Tyr	Glu	Thr	Gly	Leu	
	195					200						205				
Ala	Lys	Leu	Lys	Gly	Thr	Ser	Ala	Lys	Gln	Trp	Val	Asp	Tyr	Asn	Gln	
	210				215						220					
Phe	Arg	Arg	Glu	Met	Thr	Leu	Ala	Val	Leu	Asp	Val	Val	Ala	Leu	Phe	
225					230					235					240	
Pro	Asn	Tyr	Asp	Thr	Arg	Thr	Tyr	Pro	Met	Glu	Thr	Lys	Ala	Gln	Leu	
			245					250					255			
Thr	Arg	Glu	Val	Tyr	Thr	Asp	Pro	Leu	Gly	Ala	Val	Asn	Val	Ser	Ser	
			260					265				270				
Ile	Gly	Ser	Trp	Tyr	Asp	Lys	Ala	Pro	Ser	Phe	Gly	Val	Ile	Glu	Ser	
	275					280					285					
Ser	Val	Ile	Arg	Pro	Pro	His	Val	Phe	Asp	Tyr	Ile	Thr	Gly	Leu	Thr	
	290					295				300						
Val	Tyr	Thr	Gln	Ser	Arg	Ser	Ile	Ser	Ser	Ala	Arg	Tyr	Ile	Arg	His	
305				310						315					320	
Trp	Ala	Gly	His	Gln	Ile	Ser	Tyr	His	Arg	Val	Ser	Arg	Gly	Ser	Asn	
			325					330					335			
Leu	Gln	Gln	Met	Tyr	Gly	Thr	Asn	Gln	Asn	Leu	His	Ser	Thr	Ser	Thr	
			340					345				350				
Phe	Asp	Phe	Thr	Asn	Tyr	Asp	Ile	Tyr	Lys	Thr	Leu	Ser	Lys	Asp	Ala	
	355					360					365					
Val	Leu	Leu	Asp	Ile	Val	Tyr	Pro	Gly	Tyr	Thr	Tyr	Ile	Phe	Phe	Gly	
	370				375					380						
Met	Pro	Glu	Val	Glu	Phe	Phe	Met	Val	Asn	Gln	Leu	Asn	Asn	Thr	Arg	
385					390					395						

Ile	Val	Leu	His	Val	Asn	Asp	Ala	Gln	Ile	Gln	Met	Pro	Lys	Thr	Met
545					550					555					560
Asn	Pro	Gly	Glu	Asp	Leu	Thr	Ser	Lys	Thr	Phe	Lys	Val	Ala	Asp	Ala
				565					570						575
Ile	Thr	Thr	Leu	Asn	Leu	Ala	Thr	Asp	Ser	Ser	Leu	Ala	Leu	Lys	His
			580					585					590		
Asn	Leu	Gly	Glu	Asp	Pro	Asn	Ser	Thr	Leu	Ser	Gly	Ile	Val	Tyr	Val
		595					600					605			
Asp	Arg	Ile	Glu	Phe	Ile	Pro	Val	Asp							
	610					615									

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<220>

<223> LRMS Insert

<400> 47
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12

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<220>

<223> LRMS Insert

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